

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 22, 2002, 13:10:59 ; Search time 29 Seconds
(without alignments)
227.362 Million cell updates/sec

Title: US-09-776-781-6
Perfect score: 158
Sequence: 1 MAPTSSSTKKTQLQLEHLLKLMILNGINNY 32

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPREMBL.21.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_phage.*
- 11: sp_plant.*
- 12: sp_rodent.*
- 13: sp_virus.*
- 14: sp_vertebrate.*
- 15: sp_unclassified.*
- 16: sp_rvirus.*
- 17: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	93.0	150	4 Q9C001	Q9C001 homo sapien
2	145	91.8	154	6 Q9XS38	Q9XS38 papio hamad
3	135.5	85.8	156	4 Q13169	Q13169 homo sapien
4	134	84.8	139	4 Q16334	Q16334 homo sapien
5	108.5	68.7	155	6 Q9XT83	Q9XT83 halichoerus
6	107.5	68.0	66	6 Q9BG74	Q9BG74 canis famil
7	107	67.7	79	6 Q9TV12	Q9TV12 canis famil
8	106	67.1	155	11 Q923T2	Q923T2 sigmodon hi
9	103	65.2	138	11 Q70329	Q70329 mesocricetu
10	99	62.7	133	6 Q9WZ9R	Q9WZ9R oryctolagus
11	84	53.2	23	4 Q9UCF5	Q9UCF5 homo sapien
12	78	49.4	154	6 Q9XT84	Q9XT84 delphinapte
13	75	47.5	152	11 Q88210	Q88210 cavia porce
14	72	45.6	69	6 Q9GJRA	Q9GJRA ovis aries
15	72	45.6	155	6 Q9GL83	Q9GL83 capra hircu
16	72	45.6	155	6 Q9SKP3	Q9SKP3 bubalus bub

17	69	43.7	39	6 Q9BG73	Q9BG73 canis famil
18	69	43.7	150	11 P70291	P70291 mus musculus
19	69	43.7	169	11 Q9QUS8	Q9QUS8 mus musculus
20	67	42.4	150	11 P70294	P70294 mus musculus
21	65.5	41.5	155	11 P70292	P70292 mus musculus
22	62.5	39.6	159	11 P70293	P70293 mus musculus
23	56	35.4	300	2 Q8VW37	Q8VW37 coxiella bu
24	56	35.4	348	12 Q9DHS6	Q9DHS6 yaba-like d
25	53	33.5	251	12 Q9PYU2	Q9PYU2 xestia c-ni
26	53	33.5	452	10 Q9ZV75	Q9ZV75 arabidopsis
27	52	32.9	116	6 Q29138	Q29138 trichechus
28	52	32.9	478	17 Q8TLR6	Q8TLR6 methanosarc
29	51	32.3	517	16 Q8R6R8	Q8R6R8 thermoanaer
30	51	32.3	737	16 Q8KTG5	Q8KTG5 vibrio chol
31	51	32.3	866	16 Q25517	Q25517 helicobacte
32	51	32.3	875	16 Q9ZK28	Q9ZK28 helicobacte
33	50	31.6	95	2 Q9F8U6	Q9F8U6 streptomyce
34	50	31.6	304	16 Q930K5	Q930K5 rhizobium m
35	50	31.6	543	16 Q9KSP8	Q9KSP8 rhizobium m
36	49.5	31.3	104	10 Q9FSQ4	Q9FSQ4 oryza sativ
37	49.5	31.3	367	10 Q9SIF5	Q9SIF5 arabidopsis
38	49.5	31.3	474	10 Q06376	Q06376 brassica na
39	49	31.0	145	16 Q9KAW0	Q9KAW0 bacillus ha
40	48.5	30.7	288	16 Q99TV7	Q99TV7 staphylococ
41	48.5	30.7	366	16 Q98G42	Q98G42 rhizobium l
42	48	30.4	311	16 Q9CLL6	Q9CLL6 pasteurella
43	48	30.4	398	16 Q50911	Q50911 borrelia bu
44	48	30.4	441	16 Q928V0	Q928V0 listeria in
45	48	30.4	441	16 Q69192	Q69192 listeria mo

ALIGNMENTS

RESULT 1

ID	Q9C001	PRELIMINARY;	PRT;	150 AA.
AC	Q9C001;			
DT	01-JUN-2001 (Tremblrel. 17, Created)			
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)			
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE	Interleukin-2 (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-20545237; PubMed-11093171;			
RA	Matesanz F., Delgado C., Fresno M., Alcina A.;			
RT	"Allelic selection of human IL-2 gene."			
RL	Eur. J. Immunol. 30:3516-3521(2000).			
DR	EMBL; AF228636; AAG53575.1; -			
DR	HSSP; P01585; 3INK			
DR	InterPro; IPR000779; Interleukin-2.			
DR	Pfam; PF00715; IL2; 1.			
DR	PRINTS; PD00265; INTERLEUKIN2.			
DR	ProDom; PD003649; Interleukin-2; 1.			
DR	SMART; SM00189; IL2; 1.			
DR	PROSITE; PS00424; INTERLEUKIN_2; 1.			
FT	NON_TER			
SQ	SEQUENCE	150 AA;	17312 MW;	BF25860F8436ACE5 CRC64;

Query Match 93.0%; Score 147; DB 4; Length 150;

Best Local Similarity 96.8%; Pred. No. 4.2e-14;

Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLMILNGINNY 32

Db 21 APTSSSTKKTQLQLEHLLKLMILNGINNY 51

RESULT 2

```
Q9XS38
ID Q9XS38 PRELIMINARY; PRT; 154 AA.
AC Q9XS38;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE IL-2.
OS Papio hamadryas (Hamadryas baboon),
OS Aotus lemninus (Northern gray-necked night monkey),
OS Aotus nancymae (Owl monkey),
OS Aotus nigriceps (black-headed night monkey), and
OS Aotus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9557, 43147, 37293, 57175, 57176;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
RA Patarroyo M.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88365; AAD41538.1; -
DR EMBL; U88364; AAD41534.1; -
DR EMBL; U88361; AAD41535.1; -
DR EMBL; U88363; AAD41536.1; -
DR EMBL; U88362; AAD41537.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;

Query Match 91.8%; Score 145; DB 6; Length 154;
Best Local Similarity 93.5%; Pred. No. 8.5e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLQMLGINNY 32
   |||||
Db 21 APTSSSTKKTQLEHLLDQLMLGINNY 51
   |||||

RESULT 3
Q13169
ID Q13169 PRELIMINARY; PRT; 156 AA.
AC Q13169;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interleukin 2.
GN IL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu D., Wu Y., Chen J., Yu L., Zhong M., Hui Y., Qu H.;
RT "Expression of human IL-2 from gene transferred mouse melanoma cells
RT and its effect on the growth of mouse melanoma."
RL Chung-Hua Min kuo Wei Sheng Wu Chi Mien I Hsueh Tsa Chih
RL 13:78-82(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Xu L.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U25676; AAA70092.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.

us-09-776-781-6.rspt
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 156 AA; 18002 MW; 8E0452D43B336389 CRC64;

Query Match 85.8%; Score 135.5; DB 4; Length 156;
Best Local Similarity 88.2%; Pred. No. 2.3e-12;
Matches 30; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 2 APTSSS---TKKTQLEHLLKQLQMLGINNY 32
   |||||
Db 21 APTSSSTKKTQLEHLLDQLMLGINNY 54
   |||||

RESULT 4
Q16334
ID Q16334 PRELIMINARY; PRT; 139 AA.
AC Q16334;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE IL-2 protein (Fragment).
GN IL-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239150; PubMed=7722480;
RA Eizenberg O., Faber-Elman A., Lotan M., Schwartz M.;
RT "Interleukin-2 transcripts in human and rodent brains: possible
RT expression by astrocytes."
RL J. Neurochem. 64:1928-1936(1995).
DR EMBL; S77835; AAD14264.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15986 MW; 731FBA406D0C63C5 CRC64;

Query Match 84.8%; Score 134; DB 4; Length 139;
Best Local Similarity 90.3%; Pred. No. 3.4e-12;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLQMLGINNY 32
   |||||
Db 17 APTSSSTKKTQLEHLLDQLMLGINNY 47
   |||||

RESULT 5
Q9XT83
ID Q9XT83 PRELIMINARY; PRT; 155 AA.
AC Q9XT83;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interleukin 2.
OS Halichoerus grypus (Gray seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Halichoerus.
OX NCBI_TaxID=9711;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99221046; PubMed=10206205;
RA St-Laurent G., Beliveau C., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin
RT 2.";
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RA German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
RT "Cloning and sequencing of canine IL-2.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF091131; AAD46989.1; -
DR HSP; P01585; IIRL.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR NON_TER 1
FT 79
SQ SEQUENCE 79 AA; 9087 MW; 83079BF8F8A659BD CRC64;

Query Match 67.7%; Score 107; DB 6; Length 79;
Best Local Similarity 69.0%; Pred. No. 2.1e-08;
Matches 20; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 4 TSSSTKKTQLQLEHLLKLQMLINGINNY 32
DB 7 TSSSTKETEQQMEQLLDLDQLLLGVNYY 35

RESULT 8
Q923T2 PRELIMINARY; PRT; 155 AA.
AC Q923T2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Interleukin 2.
OS Sigmakyon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmakyon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RA Darnell M.R., Pletneva L.M., Langley R.J., Blanco J.C., Prince G.A.;
RT "Cloning, expression and purification of cotton rat IL-2.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF398549; AAK94012.1; -
DR InterPro: IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR ProDom; PD003649; Interleukin-2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; UNKNOWN_1.
DR SEQUENCE 155 AA; 17627 MW; ACAD8A865E93291 CRC64;

Query Match 67.1%; Score 106; DB 11; Length 155;
Best Local Similarity 71.0%; Pred. No. 5.8e-08;
Matches 22; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLQMLINGINNY 32
DB 21 APTSSSPKETQQLHLEQLLDQLVLLRGKNY 51

RESULT 9
O70329 PRELIMINARY; PRT; 138 AA.
ID O70329;
AC O70329;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Interleukin-2 (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=SPLEEN;
RA MEDLINE=98234044; PubMed=9573100;
RX Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis.";
RL Infect. Immun. 66:2135-2142(1998).
DR EMBL; AF046212; AAC40097.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON_TER 1
FT NON_TER 138
SQ SEQUENCE 138 AA; 15739 MW; 351032995B670779 CRC64;

Query Match 65.2%; Score 103; DB 11; Length 138;
Best Local Similarity 71.0%; Pred. No. 1.4e-07;
Matches 22; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLNGINNY 32
Db 14 APTSSSKKETQHQLEQLLDLQELKGINNY 44

RESULT 10
Q9MZR9 PRELIMINARY; PRT; 133 AA.
AC Q9MZR9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Interleukin 2 variant IL2delta2.
GN IL-2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=SPLEEN, AND LYMPH NODE;
RX MEDLINE=20304114; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RT European rabbit (Oryctolagus cuniculus).";
RL Cytokine 12:553-565(2000).
DR EMBL; AF169168; AAF86652.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 133 AA; 14748 MW; 0D54758C190B5655 CRC64;

Query Match 62.7%; Score 99; DB 6; Length 133;
Best Local Similarity 69.0%; Pred. No. 5.5e-07;
Matches 20; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLNGIN 30
Db 21 APTSSSKETQEQDQLLDLQVLLKGVN 49

RESULT 11
Q9UCF5 PRELIMINARY; PRT; 23 AA.
AC Q9UCF5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
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DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE Interleukin 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE.
RX MEDLINE=93289963; PubMed=8512072;
RA Mullner S., Karbe-Thonges B., Tripler D.;
RT "Charge heterogeneity of insulin fusion proteins expressed in
RT Escherichia coli is not due to proteolytic degradation.";
RL Anal. Biochem. 210:366-373(1993).
SQ SEQUENCE 23 AA; 2637 MW; 40B64C6875CE021F CRC64;

Query Match 53.2%; Score 84; DB 4; Length 23;
Best Local Similarity 85.7%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TSSSTKKTQLEHLLKLQML 24
Db 3 TSXSTKKTQLEHLLKLQML 23

RESULT 12
Q9XT84 PRELIMINARY; PRT; 154 AA.
AC Q9XT84;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Interleukin 2.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=99221046; PubMed=10206205;
RA St-Laurent G., Beliveau C., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) Interleukin
RT 2.";
RL Vet. Immunol. Immunopathol. 67:385-394(1999).
DR EMBL; AF072870; AAD40847.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17652 MW; 4288D3D41D04F172 CRC64;

Query Match 49.4%; Score 78; DB 6; Length 154;
Best Local Similarity 51.6%; Pred. No. 0.00088;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLNGINNY 32
Db 21 APTSSSTENTKKQVLSLLQDLHLLKEINNH 51

RESULT 13
O88210 PRELIMINARY; PRT; 152 AA.
ID O88210;
AC O88210;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Interleukin 2 precursor.
OS Cavia porcellus (Guinea pig).
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QY 2 APTSSSTKKTQLQLEHLKLTQMI LGINN 31
 ||| ||| | :: ||| ||| : |
 Db 21 APTSSSTGNTMKVEKSLDLLQLL GKVN 50

Search completed: November 22, 2002, 13:13:05
Job time : 31 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 22, 2002, 13:09:49 ; Search time 10 Seconds
(without alignments)
132.724 Million cell updates/sec

Title: US-09-776-781-6

Perfect score: 158

Sequence: 1 MAPSSSKYKTLQLEHLLKLQMLINGINNY 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	93.0	153	1 IL2_HUMAN	P01585 homo sapien
2	147	93.0	154	1 IL2_MACFA	Q29615 macaca fasc
3	147	93.0	154	1 IL2_MACMU	P51498 macaca mula
4	142	89.9	154	1 IL2_CERTO	P46649 cercocobus
5	116	73.4	154	1 IL2_MIRAN	O62641 mirounga an
6	107.5	68.0	155	1 IL2_CANFA	Q29416 canis famil
7	107	67.7	153	1 IL2_RABIT	O77620 oryctolagus
8	107	67.7	154	1 IL2_FELCA	Q07885 felis silve
9	97	61.4	155	1 IL2_RAT	P17108 rattus norv
10	96	60.8	154	1 IL2_PIG	P26891 sus scrofa
11	95	60.1	155	1 IL2_MERUN	Q08081 meriones un
12	88	55.7	152	1 IL2_ORCOR	O97513 orcinus orc
13	85	53.8	149	1 IL2_HORSE	P37997 equus cabal
14	72	45.6	155	1 IL2_BOVIN	P05016 bos taurus
15	72	45.6	155	1 IL2_CAPHI	P36835 capra hircu
16	72	45.6	155	1 IL2_SHEEP	P19114 ovis aries
17	72	45.6	162	1 IL2_CEREL	P51747 cervus elap
18	64.5	40.8	166	1 IL2_MUSSP	Q08867 mus spretus
19	64	40.5	169	1 IL2_MOUSE	P04351 mus musculu
20	61	38.6	189	1 Y064_METJA	Q60376 methanococc
21	56	35.4	1046	1 POL_SIVAG	P27980 simian immu
22	54	34.2	1061	1 POL_SIVAT	P05895 simian immu
23	53	33.5	357	1 AAAA_EMENI	P21133 emericella
24	51.5	32.6	415	1 CGA2_XENLA	P47827 xenopus lae
25	51	32.3	746	1 PCAP_HUMAN	Q96rn5 mus sapien
26	51	32.3	792	1 PCAP_MOUSE	Q924h2 mus musculu
27	50.5	32.0	741	1 RN5A_HUMAN	Q05823 homo sapien
28	48.5	30.7	452	1 TRPC_HELPY	Q02867 helicobacte
29	47.5	30.1	150	1 RNK6_SAISS	O46529 salminki sci
30	47.5	30.1	150	1 RNK6_BOVIN	P08904 bos taurus
31	47	29.7	257	1 ABCX_GALSU	P35020 galdieria s
32	47	29.7	406	1 CBG2_BOVIN	P30274 bos taurus
33	47	29.7	421	1 CGA2_MOUSE	Q61456 mus musculu

ALIGNMENTS

RESULT 1

ID	IL2_HUMAN	STANDARD	PRT	153 AA
AC	P01585			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)			
DE	(Aldelesleukin).			
GN	IL2.			
OS	Homo sapiens (Human), and			
OS	Hylobates lar (Common gibbon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606, 9580;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=84247353; PubMed=6330695;			
RA	Holbrook N.J., Lieber M., Crabtree G.R.;			
RT	"DNA sequence of the 5' flanking region of the human interleukin 2			
RT	gene: homologies with adult T-cell leukemia virus.;"			
RL	Nucleic Acids Res. 12:5005-5013(1984).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=83167472; PubMed=6403867;			
RA	Taniguchi T., Matsui H., Fujita T., Takaoka C., Kashima N.,			
RA	Yoshimoto R., Hamuro J.;			
RT	"Structure and expression of a cloned cDNA for human interleukin-2.;"			
RL	Nature 302:305-310(1983).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=84023840; PubMed=6312994;			
RA	Maeda S., Nishino N., Obaru K., Mita S., Nomiyama H., Shimada K.,			
RA	Fujimoto K., Teranishi T., Hirano T., Onoue K.;			
RT	"Cloning of interleukin 2 mRNAs from human tonsils.;"			
RL	Biochem. Biophys. Res. Commun. 115:1040-1047(1983).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=83246551; PubMed=6306584;			
RA	Devos R., Plaetinck G., Cheroutre H., Simons G., Degraeve W.,			
RA	Tavernier J., Remaut E., Fiers W.;			
RT	"Molecular cloning of human interleukin 2 cDNA and its expression in			
RT	E. coli.;"			
RL	Nucleic Acids Res. 11:4307-4323(1983).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=84170356; PubMed=6608729;			
RA	Holbrook N.J., Smith K.A., Fornace A.J. Jr., Comeau C.M.,			
RA	Wiskocil R.L., Crabtree G.R.;			
RT	"T-cell growth factor: complete nucleotide sequence and organization			
RT	of the gene in normal and malignant cells.;"			

34	47	29.7	432	1	CGA2_HUMAN	P20248 homo sapien
35	47	29.7	465	1	CGA1_HUMAN	P78396 homo sapien
36	47	29.7	943	1	YLW5_CAEEL	P34408 caenorhabdi
37	47	29.7	1492	1	CFTR_SOUAC	P26362 squalus aca
38	46.5	29.4	989	1	T100_HUMAN	O75448 homo sapien
39	46	29.1	532	1	G6PI_BORBU	O51672 borrelia bu
40	46	29.1	1403	1	PRO_DRONE	P29617 drosophila
41	45	28.5	81	1	EX7S_PASMU	Q9cna0 pasteurella
42	45	28.5	155	1	YHCH_HAEIN	P44403 haemophilus
43	45	28.5	351	1	YNX1_YEAST	P53860 saccharomyc
44	45	28.5	368	1	LEU3_NEUCR	P34738 neurospora
45	45	28.5	479	1	ZW10_DROPS	O44218 drosophila

RL PROC. Natl. Acad. Sci. U.S.A. 81:1634-1638(1984).
 RP [6]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=84170243; PubMed=6324170;
 RA Fujita T., Takaoaka C., Matsui H., Taniguchi T.;
 RT "Structure of the human interleukin 2 gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:7437-7441(1983).
 RN [7]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=95239150; PubMed=7722480;
 RA Eizenberg O., Faber-Elman A., Lotan M., Schwartz M.;
 RT "Interleukin-2 transcripts in human and rodent brains: possible
 expression by astrocytes.";
 RL J. Neurochem. 64:1928-1936(1995).
 RN [8]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Placenta;
 RX MEDLINE=96422299; PubMed=8824916;
 RA Chernicky C.L., Tan H., Burfeind P., Ilan J., Ilan J.;
 RT "Sequence of Interleukin-2 isolated from human placental poly A+ RNA:
 possible role in maintenance of fetal allograft.";
 RL Mol. Reprod. Dev. 43:180-186(1996).
 RN [9]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=87064618; PubMed=3491296;
 RA Sliedenlist U., Durand D.B., Bressler P., Holbrook N.J., Norris C.A.,
 RA Ramoun M., Kant J.A., Crabtree G.R.;
 RT "Promoter region of interleukin-2 gene undergoes chromatin structure
 changes and confers inducibility on chloramphenicol acetyltransferase
 gene during activation of T cells.";
 RL Mol. Cell. Biol. 6:3042-3049(1986).
 RN [12]
 RN SEQUENCE OF 1-68 FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=85038540; PubMed=6333684;
 RA Robb R.J., Kutny R.M., Panico M., Morris H.R., Chowdhry V.;
 RT "Amino acid sequence and post-translational modification of human
 interleukin 2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:6486-6490(1984).
 RN [14]
 RN CARBOHYDRATE-LINKAGE SITE.
 RC SPECIES=Human;
 RX MEDLINE=90008901; PubMed=2793860;
 RA Conradt H.S., Nimtz M., Dittmar K.E.J., Lindenmaier W., Hoppe J.,
 RA Hauser H.;
 RT "Expression of human interleukin-2 in recombinant baby hamster
 kidney, Ltk+, and Chinese hamster ovary cells. Structure of O-linked
 carbohydrate chains and their location within the polypeptide.";
 RL J. Biol. Chem. 264:17368-17373(1989).

RN SEQUENCE FROM N.A.
 RC SPECIES=H.lar;
 RX MEDLINE=86042650; PubMed=3877307;
 RA Chen S.J., Holbrook N.J., Mitchell K.F., Vallone C.A.,
 RA Greengard J.S., Crabtree G.R., Lin Y.;
 RT "A viral long terminal repeat in the interleukin 2 gene of a cell
 line that constitutively produces interleukin 2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7284-7288(1985).
 RN [16]
 RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RC SPECIES=Human;
 RX MEDLINE=88070646; PubMed=3500515;
 RA Brandhuber B.J., Boone T., Kenney W.C., McKay D.B.;
 RT "Three-dimensional structure of interleukin-2.";
 RL Science 238:1707-1709(1987).
 RN [17]
 RN X-RAY CRYSTALLOGRAPHY.
 RC SPECIES=Human;
 RX MEDLINE=92335891; PubMed=1631562;
 RA Bazan J.F.;
 RT "Unravelling the structure of IL-2.";
 RL Science 257:410-412(1992).
 RN [18]
 RN RESPONSE TO ABOVE LETTER.
 RA McKay D.B.;
 RL Science 257:412-413(1992).
 RN [19]
 RN STRUCTURE BY NMR.
 RX MEDLINE=92379010; PubMed=1510960;
 RA Mott H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P.,
 RA Campbell I.D.;
 RT "Secondary structure of human interleukin 2 from 3D heteronuclear NMR
 experiments.";
 RL Biochemistry 31:7741-7744(1992).
 RN [20]
 RN 3D-STRUCTURE MODELING.
 RX MEDLINE=95111955; PubMed=7529123;
 RA Bamorough P., Hedgecock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 modelling.";
 RL Structure 2:839-851(1994).
 CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
 MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
 PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
 IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
 ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
 WHICH INVOLVES IL2 AND BCMA.
 CC -!- PHARMACEUTICAL: Available under the name Proleukin (Chiron). Used
 in patients with renal cell carcinoma or metastatic melanoma.
 CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
 CC -!- DATABASE: NAME-RED Systems' cytokine source book: IL2;
 WWW="http://www.fndsystems.com/asp/g-sitebuilder.asp?bodyId=206".
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 CC -----
 DR EMBL: J00264; A048509.1; -
 DR EMBL: X01586; CAA25742.1; -
 DR EMBL: V00564; CAA23827.1; -
 DR EMBL: X00695; CAA25292.1; -
 DR EMBL: K02056; AAA98792.1; -
 DR EMBL: M13879; AAA59141.1; -
 DR EMBL: X03174; AAA35453.1; -
 DR EMBL: S77834; A014263.2; -
 DR EMBL: S62692; A046883.1; -


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Query Match          93.0%; Score 147; DB 1; Length 153;
Best Local Similarity 96.8%; Pred. No. 5.8e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLHLKLQMLINGINNY 32
DB 21 APTSSSTKKTQLEHLHLKLQMLINGINNY 51

RESULT 2
IL2_MACFA          STANDARD;          PRT;          154 AA.
AC Q29615;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Yabe M., Matsuura Y., Tatsumi M.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; D63352; BAA09676.1; -.
DR HSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00285; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL          1 20 BY SIMILARITY.
FT CHAIN           21 154 INTERLEUKIN-2.
FT CARBOHYD        23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID        78 126 BY SIMILARITY.
SQ SEQUENCE 154 AA; 17686 MW; 7853FE624A5E4A49 CRC64;

Query Match          93.0%; Score 147; DB 1; Length 154;
Best Local Similarity 96.8%; Pred. No. 5.8e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLHLKLQMLINGINNY 32
DB 21 APTSSSTKKTQLEHLHLKLQMLINGINNY 51

RESULT 3
IL2_MACMU          STANDARD;          PRT;          154 AA.
AC P51498;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Macaca mulatta (Rhesus macaque), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RL MEDLINE=96003435; PubMed=7561102;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
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CC -----
DR EMBL; U19847; AAB60400.1; -.
DR EMBL; U19852; AAA86714.1; -.
DR HSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00285; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL          1 20 BY SIMILARITY.
FT CHAIN           21 154 INTERLEUKIN-2.
FT CARBOHYD        23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID        78 126 BY SIMILARITY.
SQ SEQUENCE 154 AA; 17685 MW; 6AEB480F204BA49 CRC64;

Query Match          93.0%; Score 147; DB 1; Length 154;
Best Local Similarity 96.8%; Pred. No. 5.8e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLHLKLQMLINGINNY 32
DB 21 APTSSSTKKTQLEHLHLKLQMLINGINNY 51

RESULT 4
IL2_CERTO          STANDARD;          PRT;          154 AA.
AC P46649;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
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OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercocebus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC
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CC
CC EMBL; U19846; AAB50399.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
FT VARIANT 25 25 R -> S.
FT VARIANT 74 74 K -> E.
SQ SEQUENCE 154 AA; 17754 MW; 9FEB51814204BA48 CRC64;

Query Match 89.9%; Score 142; DB 1; Length 154;
Best Local Similarity 93.5%; Pred. No. 3.3e-14;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLMILNGINNY 32
Db 21 APTSRSTKKTQLEHLLKQLMILNGINNY 51
|||||
RESULT 5
IL2_MIRAN STANDARD; PRT; 154 AA.
AC O62641;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Mirounga angustirostris (Northern elephant seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Mirounga.
OX NCBI_TaxID=9716;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98136706; PubMed=9476229;
RA Shoda L.K.M., Brown W.C., Rice-Ficht A.C.;

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RT "Sequence and characterization of phocine interleukin 2.";
RL J. Wildl. Dis. 34:81-90(1998).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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CC
CC EMBL; U79187; AAC12258.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
FT SEQUENCE 154 AA; 17661 MW; 0C92337A4B16B6BB CRC64;

Query Match 73.4%; Score 116; DB 1; Length 154;
Best Local Similarity 71.0%; Pred. No. 2.6e-10;
Matches 22; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLMILNGINNY 32
Db 21 APTSSSTKKTQLEHLLKQLMILNGINNY 51
|||||
RESULT 6
IL2_CANFA STANDARD; PRT; 155 AA.
ID IL2_CANFA
AC Q29416; Q28249;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=XBRED21/12/93; TISSUE=Lymph node;
RX MEDLINE=95337423; PubMed=7612930;
RA Dunham S.P., Argyle D.J., Onions D.E.;
RT "The isolation and sequence of canine interleukin-2.";
RL DNA Seq. 5:177-180(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96016696; PubMed=8571541;
RA Somberg R.L., Pullen R.P., Casal M.L., Patterson D.F., Felsburg P.J.,
RA Henthorn P.S.;
RT "A single nucleotide insertion in the canine interleukin-2 receptor
RT gamma chain results in X-linked severe combined immunodeficiency
RT disease.";
RL Vet. Immunol. Immunopathol. 47:203-213(1995).

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[3]
RN SEQUENCE FROM N.A.
RP STRAIN=Beagle; TISSUE=Spleen;
RX MEDLINE=95347614; PubMed=7622066;
RA Knapp D.W., Williams J.S., Andrisani O.M.;
RT "Cloning of the canine interleukin-2 encoding cDNA.";
RL Gene 159:281-282(1995).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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CC
CC EMBL: D30710; BAA06378.1; -
CC EMBL: U28141; AAB68969.1; -
CC EMBL: U11689; AAB75360.1; -
CC HSP: P01585; 3INK.
CC InterPro: IPR000779; Interleukin-2.
CC Pfam: PF00715; IL2; 1.
CC PRINTS: PR00265; INTERLEUKIN2.
CC ProDom: PD003649; Interleukin-2; 1.
CC SMART: SM00189; IL2; 1.
CC PROSITE: PS00424; INTERLEUKIN_2; 1.
CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
CC T-cell.
CC
CC SIGNAL 1 20 BY SIMILARITY.
CC CHAIN 21 155 INTERLEUKIN-2.
CC CARBOHYD 24 24 O-LINKED (GLNAC. . .) (BY SIMILARITY).
CC FT CARBOHYD 112 112 N-LINKED (GLNAC. . .) (POTENTIAL).
CC FT DISULFID 79 127 BY SIMILARITY.
CC FT CONFLICT 4 4 M -> I (IN REF. 3).
CC FT CONFLICT 37 37 Q -> R (IN REF. 3).
CC FT CONFLICT 151 151 F -> Y (IN REF. 3).
CC FT CONFLICT 154 154 L -> X (IN REF. 3).
CC SEQUENCE 155 AA; 17668 MW; D123E486B7F4AC1D CRC64;

Query Match 68.0%; Score 107.5; DB 1; Length 155;
Best Local Similarity 68.8%; Pred. No. 4.9e-09;
Matches 22; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

OY 2 AP-TSSSTKTKQLQLPQLHLLKLQMLINGNNY 32
|| |||||:|:|:| |||||:|:|:|
Db 21 APITSSSTKETEQQEQQLLDQLLLGNGVNY 52

RESULT 7
IL2_RABIT
ID IL2_RABIT STANDARD; PRT; 153 AA.
AC Q77620;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RX MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;

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RT "The complete cDNA sequences of IL-2, IL-4, IL-6 AND IL-10 from the
RT European rabbit (Oryctolagus cuniculus).";
RL Cytokine 12:555-565(2000).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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CC
CC EMBL: AF068057; AAC23838.1; -
CC HSP: P01585; 3INK.
CC InterPro: IPR000779; Interleukin-2.
CC Pfam: PF00715; IL2; 1.
CC PRINTS: PR00265; INTERLEUKIN2.
CC ProDom: PD003649; Interleukin-2; 1.
CC SMART: SM00189; IL2; 1.
CC PROSITE: PS00424; INTERLEUKIN_2; 1.
CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
CC T-cell.
CC
CC SIGNAL 1 20 BY SIMILARITY.
CC CHAIN 21 153 INTERLEUKIN-2.
CC CARBOHYD 23 23 O-LINKED (GLNAC. . .) (BY SIMILARITY).
CC FT CARBOHYD 111 111 N-LINKED (GLNAC. . .) (POTENTIAL).
CC FT DISULFID 78 125 BY SIMILARITY.
CC SEQUENCE 153 AA; 17256 MW; 8173536B2DD8B86 CRC64;

Query Match 67.7%; Score 107; DB 1; Length 153;
Best Local Similarity 67.7%; Pred. No. 5.8e-09;
Matches 21; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 2 APTSSSTKTKQLQLHLLKLQMLINGNNY 32
|| |||||:|:|:| |||||:|:|:|
Db 21 APITSSSTKETEQQEQQLLDQLLLGNGVNDY 51

RESULT 8
IL2_FELCA
ID IL2_FELCA STANDARD; PRT; 154 AA.
AC Q07885;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93356765; PubMed=8352761;
RA Cozzi P.J., Padrid P.A., Takeda J., Alegre M.-A., Yuhki N.,
RA Leff A.R.;
RT "Sequence and functional characterization of feline interleukin 2.";
RL Biochem. Biophys. Res. Commun. 194:1038-1043(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Litman R., Gibbs C., Good R.A., Day N.K.;
RA Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-

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CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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CC -----
CC EMBL: L19402; AAA02865.1; -.
CC DR EMBL: L25408; AAA51431.1; -.
CC DR PIR: JN0698; JN0698.
CC DR HSSP: P01585; 3INK.
CC DR InterPro: IPR000779; Interleukin-2.
CC DR PRINTS: PR00265; INTERLEUKIN2.
CC DR ProDom: PD003649; Interleukin-2; 1.
CC DR SMART: SM00189; IL2; 1.
CC DR PROSITE: PS00424; INTERLEUKIN_2; 1.
CC DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
CC KW T-cell.
CC FT SIGNAL 1 20 BY SIMILARITY.
CC FT CHAIN 21 154 INTERLEUKIN-2.
CC FT DISULFID 78 126 BY SIMILARITY.
CC FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFLICT 3 4 KI -> RM (IN REF. 2).
CC FT CONFLICT 150 150 F -> I (IN REF. 2).
CC FT SEQUENCE 154 AA; 17653 MW; 2E71E3BD8B9665EF CRC64;
CC Query Match 67.7%; Score 107; DB 1; Length 154;
CC Best Local Similarity 70.0%; Pred. No. 5.8e-09;
CC Matches 21; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
CC -----
CC QY 2 APTSSSTKTKTQLEHLLKQLMILNGINN 31
CC II IIIII:II III III I:::IIII:II
CC Db 21 APASSTKETQQQLQLLDRLRLNGVNN 50
CC -----
CC RESULT 9
CC IL2_RAT
CC ID IL2_RAT STANDARD; PRT; 155 AA.
CC AC P17108;
CC DT 01-AUG-1990 (Rel. 15, Created)
CC DT 01-AUG-1990 (Rel. 15, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
CC GN IL2 OR IL-2.
CC OS Rattus norvegicus (Rat).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC OX NCBI_TaxID=10116;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=89339608; PubMed=2788130;
CC RA McKnight A.J., Mason D.W., Barclay A.N.;
CC RT "Sequence of rat interleukin 2 and anomalous binding of a mouse
CC RT interleukin 2 cDNA probe to rat MHC class II-associated invariant
CC RT chain mRNA.";
CC RL Immunogenetics 30:145-147(1989).
CC CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC CC -!- SUBCELLULAR LOCATION: Secreted.
CC CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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CC -----
CC EMBL: M22899; AAA41427.1; -.
CC DR PIR: A31278; A31278.
CC DR PIR: A45882; A45882.
CC DR HSSP: P01585; 3INK.
CC DR InterPro: IPR000779; Interleukin-2.
CC DR Pfam: PF00715; IL2; 1.
CC DR PRINTS: PR00265; INTERLEUKIN2.
CC DR ProDom: PD003649; Interleukin-2; 1.
CC DR SMART: SM00189; IL2; 1.
CC DR PROSITE: PS00424; INTERLEUKIN_2; 1.
CC DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
CC KW T-cell.
CC FT SIGNAL 1 20 BY SIMILARITY.
CC FT CHAIN 21 155 INTERLEUKIN-2.
CC FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
CC FT DISULFID 78 126 BY SIMILARITY.
CC FT SEQUENCE 155 AA; 17632 MW; 67A8554A73BF30A0 CRC64;
CC Query Match 61.4%; Score 97; DB 1; Length 155;
CC Best Local Similarity 64.5%; Pred. No. 1.9e-07;
CC Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
CC -----
CC QY 2 APTSSSTKTKTQLEHLLKQLMILNGINN 32
CC IIIII:II III III I:::IIII:II
CC Db 21 APTSSPAKETQQHLEQLLDQLVLLRGIDNY 51
CC -----
CC RESULT 10
CC IL2_PIG
CC ID IL2_PIG STANDARD; PRT; 154 AA.
CC AC P26891;
CC DT 01-AUG-1992 (Rel. 23, Created)
CC DT 01-AUG-1992 (Rel. 23, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
CC GN IL2.
CC OS Sus scrofa (Pig).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CC OX NCBI_TaxID=9823;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=T-cell;
CC RX MEDLINE=91274360; PubMed=2054386;
CC RA Goodall J.C., Emery D.C., Bailey M., English L.S., Hall L.;
CC RT "cDNA cloning of porcine interleukin 2 by polymerase chain reaction.";
CC RL Biochim. Biophys. Acta 1089:257-258(1991).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=T-cell;
CC RA Lefevre F.;
CC RL Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
CC RN [3]
CC RP SEQUENCE FROM N.A.
CC RA Iwata H., Hasegawa A., Yamamoto M., Oida T., Endo Y., Inoue T.;
CC RT "Structure of the porcine chromosomal interleukin-2 gene.";
CC RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC CC -!- SUBCELLULAR LOCATION: Secreted.
CC CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 >152 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
FT NON_TER 152 152
SQ SEQUENCE 152 AA; 17424 MW; 308991821ECCB764 CRC64;

Query Match 55.7%; Score 88; DB 1; Length 152;
Best Local Similarity 58.1%; Pred. No. 4.le-06;
Matches 18; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 2 APTSSSTKTKQLQLEHLLKLMILNGINN 32
| | | | | : : : : | | | | |
Db 21 APTSSSTNTKKQVQSLLQDLQLLLKEINNY 51

RESULT 13
IL2_HORSE
ID IL2_HORSE STANDARD; PRT; 149 AA.
AC P37997;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OC NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94160538; PubMed=8116217;
RA Vandergriff E.V., Horohov D.W.;
RT "Molecular cloning and expression of equine interleukin 2.";
RL Vet. Immunol. Immunopathol. 39:395-406(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Tavernor A.S., Allen W.R., Butcher G.W.;
RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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CC -----
DR EMBL; L06009; AAA20134.1; -
DR EMBL; X69393; CAA49190.1; -
DR PIR; S31391; S31391.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 149 INTERLEUKIN-2.
FT DISULFID 78 121 BY SIMILARITY.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT CARBOHYD 106 106 N-LINKED (GLUCNAC. . .) (POTENTIAL).
FT CARBOHYD 3 3 R -> K (IN REF. 2).
FT CONFLICT 3 3
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FT CONFLICT 8 8 S -> A (IN REF. 2).
FT CONFLICT 59 59 I -> M (IN REF. 2).
FT CONFLICT 125 125 N -> D (IN REF. 2).
FT CONFLICT 128 128 E -> G (IN REF. 2).
FT CONFLICT 145 145 I -> F (IN REF. 2).
FT CONFLICT 148 148 L -> M (IN REF. 2).
SQ SEQUENCE 149 AA; 17086 MW; 051BB8C47A0114FC CRC64;

Query Match 53.8%; Score 85; DB 1; Length 149;
Best Local Similarity 53.3%; Pred. No. 1.le-05;
Matches 16; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 2 APTSSSTKTKQLQLEHLLKLMILNGINN 31
| | | | | : : : | | | : : : | | |
Db 21 APTSSSKRETTQQLKQLMDLKLLEGVNN 50

RESULT 14
IL2_BOVIN
ID IL2_BOVIN STANDARD; PRT; 155 AA.
AC P05016;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2 OR IL-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86205869; PubMed=3517854;
RA Cerretti D.P., McKereghan K., Larsen A., Cantrell M.A., Anderson D.,
RA Gillis S., Cosman D., Baker P.E.;
RT "Cloning, sequence, and expression of bovine interleukin 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3223-3227(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86205870; PubMed=3486415;
RA Reeves R., Spies A.G., Nissen M.S., Buck C.D., Weinberg A.D.,
RA Barr P.J., Magnuson N.S., Magnuson J.A.;
RT "Molecular cloning of a functional bovine interleukin 2 cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3228-3232(1986).
RN [3]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Thymus;
RA Anikeeva N.N., Vinogradova T.V., Votoshin O.N.;
RL Submitted (DEC-1989) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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CC -----
DR EMBL; M12791; AAA30586.1; -
DR EMBL; M13204; AAA21143.1; ALT_INIT.
DR EMBL; X17201; CAA35062.1; -
DR EMBL; X52687; CAA36912.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
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Search completed: November 22, 2002, 13:11:47
Job time : 11 secs

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OM protein - protein search, using sw model

Run on: November 22, 2002, 13:11:19 : Search time 15 Seconds
(without alignments)
205.087 Million cell updates/sec

Title: US-09-776-781-6
Perfect score: 158
Sequence: 1 MAPTSSSTKTKQLQLHLLKLQMLINGINNY 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73 : *
1: pir1 : *
2: pir2 : *
3: pir3 : *
4: pir4 : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	93.0	153	1 ICHU2	interleukin-2 prec
2	147	93.0	153	1 ICG12	interleukin-2 prec
3	107	67.7	154	2 JN0698	interleukin-2 prec
4	97	61.4	155	2 A31278	interleukin-2 prec
5	96	60.8	154	2 S16241	interleukin-2 prec
6	95	60.1	155	2 S33509	interleukin-2 - Mo
7	85	53.8	149	2 S31391	interleukin-2 prec
8	72	45.6	155	2 S38662	interleukin-2 - go
9	72	45.6	155	2 S11488	interleukin-2 prec
10	72	45.6	155	2 I45913	interleukin-2 prec
11	69	43.7	169	2 S37289	interleukin-2 prec
12	64	40.5	169	1 ICWS52	interleukin-2 prec
13	61	38.6	189	2 H64307	hypothetical prote
14	54	34.2	1061	1 GNLJG4	HIV-1 retropepsin
15	53	33.5	357	2 S12169	isopenicillin N ac
16	53	33.5	452	2 B84483	hypothetical prote
17	52.5	33.2	60	2 I68870	interleukin 2 - we
18	51.5	32.6	62	2 I54512	interleukin 2 - mo
19	51.5	32.6	415	2 I51637	cyclin A2 - Africa
20	51	32.3	737	2 G82262	probable exopolysa
21	51	32.3	866	2 F64625	type I restriction
22	51	32.3	875	2 B71890	type I restriction
23	50.5	32.0	72	2 I68871	interleukin 2 - mo
24	50.5	32.0	741	2 A45771	2-5A-dependent RNA
25	50	31.6	304	2 F95285	probable LysR-type
26	50	31.6	543	2 F82217	methyl-accepting c
27	49.5	31.3	367	2 E84453	probable GDSL-moti
28	49.5	31.3	474	2 S31712	beta-1,3-glucanase
29	49	31.0	145	2 H83921	transcription regu

30	48.5	30.7	288	2 B89930	hypothetical prote
31	48.5	30.7	452	2 G64679	anthranilate isome
32	48	30.4	398	2 B70209	conserved hypothet
33	48	30.4	441	2 AB1367	aminopeptidase C I
34	48	30.4	441	2 AC1736	hypothetical prote
35	48	30.4	765	2 S76795	hypothetical prote
36	48	30.4	1964	2 A59282	nonmuscle myosin I
37	47.5	30.1	127	1 NR80K2	pancreatic-type ri
38	47.5	30.1	244	2 T11685	hypothetical prote
39	47	29.7	257	2 S39521	hypothetical prote
40	47	29.7	307	2 T46103	hypothetical prote
41	47	29.7	406	2 S24788	cyclin A - bovine
42	47	29.7	432	2 S08277	cyclin A - human
43	47	29.7	511	2 D71687	alkaline proteinas
44	47	29.7	531	2 T33319	hypothetical prote
45	47	29.7	564	2 S76672	hypothetical prote

ALIGNMENTS

RESULT 1

ICHU2
Interleukin-2 precursor [validated] - human
N:Alternate names: IL-2; T-cell growth factor
C:Species: Homo sapiens (man)
C:Date: 11-Aug-1983 #sequence_revision 11-Aug-1983 #text_change 08-Dec-2000
C:Accession: A01849; A21192; A20961; S31209; A93297; A90113; A93478; I56518; I73624;
R:Holbrook, N.J.; Lieber, M.; Crabtree, G.R.
Nucleic Acids Res. 12, 5005-5013, 1984
A:Title: DNA sequence of the 5' flanking region of the human interleukin 2 gene: homo
A:Reference number: A93524; MUID:84247353; PMID:6330895
A:Accession: A01849
A:Molecule type: DNA
A:Residues: 1-153 <HOL>
A:Cross-references: GB:X00695; GB:X00200; GB:X00201; GB:X00202; NID:g33783; PIDN:CAA2
R:Fujita, T.; Takaoka, C.; Matsui, H.; Taniguchi, T.
Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983
A:Title: Structure of the human interleukin 2 gene.
A:Reference number: A21192; MUID:84170243; PMID:6324170
A:Accession: A21192
A:Molecule type: DNA
A:Residues: 1-153 <PUJ>
A:Cross-references: GB:J00264; NID:gl86294; PIDN:AAD48509.1; PID:g5729676
R:Holbrook, N.J.; Smith, K.A.; Fornace Jr., A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabt
Proc. Natl. Acad. Sci. U.S.A. 81, 1634-1638, 1984
A:Title: T-cell growth factor: complete nucleotide sequence and organization of the g
A:Reference number: A20961; MUID:84170356; PMID:6608729
A:Accession: A20961
A:Molecule type: DNA
A:Residues: 1-153 <HO2>
A:Cross-references: GB:K02056; NID:gl86302; PIDN:AAA98792.1; PID:g386819
R:Laabl, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapi
EMBO J. 11, 3897-3904, 1992
A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(
A:Reference number: S31208; MUID:93010984; PMID:1396583
A:Accession: S31209
A:Molecule type: mRNA
A:Residues: 11-117 <LAA>
A:Cross-references: EMBL:Z14955
A:Note: this sequence is shown from the beginning of the fragment to the chromosomal
R:Taniguchi, T.; Matsui, H.; Fujita, T.; Takaoka, C.; Kashima, N.; Yoshimoto, R.; Ham
Nature 302, 305-310, 1983
A:Title: Structure and expression of a cloned cDNA for human interleukin-2.
A:Reference number: A93297; MUID:83167472; PMID:6403867
A:Accession: A93297
A:Molecule type: mRNA
A:Residues: 1-153 <TAN>
A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781
A:Experimental source: Leukemic T-cell line, Jurkat-111, cloned from Jurkat-FHCRC
R:Maeda, S.; Nishino, N.; Obaru, K.; Mita, S.; Nomiya, H.; Shimada, K.; Fujimoto, K
Biochem. Biophys. Res. Commun. 115, 1040-1047, 1983
A:Title: Cloning of interleukin 2 mRNAs from human tonsils.

A:Reference number: A90113; MUID:84023840; PMID:6312994
A:Accession: A90113
A:Molecule type: mRNA
A:Residues: 1-153 <MAE>
A:Cross-references: GB:J00264; NID:g186294; PIDN:AA48509.1; PID:g5729676
A:Experimental source: tonsillar mononuclear cells
R:Devois, R.; Plactinck, G.; Cheroutre, H.; Simons, G.; Degraeve, W.; Tavernier, J.; Remau
Nucleic Acids Res. 11, 4307-4323, 1983
A:Title: Molecular cloning of human interleukin 2 cDNA and its expression in Escherichia
A:Reference number: A93478; MUID:83246551; PMID:6306584
A:Accession: A93478
A:Molecule type: mRNA
A:Residues: 1-153 <DEV>
A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781
A:Experimental source: splenocytes
R:Elzenberg, O.; Faber-Elman, A.; Lotan, M.; Schwartz, M.
J. Neurochem. 64, 1928-1936, 1995
A:Title: Interleukin-2 transcripts in human and rodent brains: possible expression by as
A:Reference number: I56518; MUID:95239150; PMID:7722480
A:Accession: I56518
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-152 <EIZ>
A:Cross-references: GB:S77834; NID:g999000
A:Accession: I73624
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 5-7,'F','9-17','p','19-32','X','34-45','X','47-143 <RES>
A:Cross-references: GB:S77835; NID:g999001; PIDN:AA414264.1; PID:g4261964
R:Nishino, N.; Obaru, K.; Maeda, S.; Shimada, K.; Onoue, K.
Biomed. Res. 6, 197-205, 1985
A:Title: Organization of the DNA regions flanking the human interleukin 2 gene.
A:Reference number: I52528
A:Accession: I52528
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-68 <REZ>
A:Cross-references: GB:M33199; NID:g186296; PIDN:AA59139.1; PID:g553508
R:Siebenlist, U.; Durand, D.B.; Bressler, P.; Holbrook, N.J.; Norris, C.A.; Kamoun, M.;
Mol. Cell. Biol. 6, 3042-3049, 1986
A:Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes and
A:Reference number: I57603; MUID:87064618; PMID:3491296
A:Accession: I57603
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-68 <RE3>
A:Cross-references: GB:M13879; NID:g186305; PIDN:AA59141.1; PID:g553509
R:Weir, M.P.; Chaplin, M.A.; Wallace, D.M.; Dykes, C.W.; Hobden, A.N.
Biochemistry 27, 6883-6892, 1988
A:Title: Structure-activity relationships of recombinant human interleukin 2.
A:Reference number: I52401; MUID:89062420; PMID:3264184
A:Contents: recombinant IL-2 and mutants expressed in E. coli
A:Accession: I52401
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 'M','21-153 <RE4>
A:Cross-references: GB:M22005; NID:g186300; PIDN:AA59140.1; PID:g386818
A:Note: mutation of Phe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold without
R:Robb, R.J.; Kutny, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V.
Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984
A:Title: Amino acid sequence and post-translational modification of human interleukin 2.
A:Reference number: A94009; MUID:85038540; PMID:6333684
A:Accession: A94009
A:Molecule type: protein
A:Residues: 21-153 <ROB>
A:Note: disulfide bonds and carbohydrate binding site were determined
A:Note: heterogeneity in Jurkat-derived IL-2 is primarily due to differences in glycosyl
n in lacking 21-Ala (FT-IL2-A and FT-IL2-B) and 22-Pro (FT-IL2-B)
R:Conradt, H.S.; Nimtz, M.; Dittmar, K.E.J.; Lindenmaier, W.; Hoppe, J.; Hauser, H.
J. Biol. Chem. 264, 17368-17373, 1989
A:Title: Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk-, and
de.
A:Reference number: A34463; MUID:90008901; PMID:2793860

A:Accession: A34463
A:Molecule type: protein
A:Residues: 21-35 <CON>
A:Note: the O-linked glycosylation site in recombinant material matched that from hum
R:Grabenhorst, E.; Hofer, B.; Nimtz, M.; Jaeger, V.; Conradt, H.S.
Eur. J. Biochem. 215, 189-197, 1993
A:Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants fro
A:Reference number: S34052; MUID:93345493; PMID:8344280
A:Contents: annotation; glycosylation of variant forms expressed in insect cells
C:Genetics:
A:Gene: GDB:IL2
A:Cross-references: GDB:119344; OMIM:147680
A:Map position: 4q26-4q27
A:Introns: 49/3; 69/3; 117/3
C:Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-153/Product: interleukin-2 #status experimental <IL2>
F:23/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:78-125/Disulfide bonds: #status experimental
Query Match 93.0%; Score 147; DB 1; Length 153;
Best Local Similarity 96.8%; Pred. No. 7.4e-14;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 APTSSSTKKTQLEHLLKLQMLNGINNY 32
Db 21 APTSSSTKKTQLEHLLKLQMLNGINNY 51
RESULT 2
ICG12
interleukin-2 precursor - common gibbon
N:Alternate names: IL-2; T-cell growth factor
C:Species: Hylobates lar (common gibbon, white-handed gibbon)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
C:Accession: A94067; A01849
R:Chen, S.J.; Holbrook, N.J.; Mitchell, K.F.; Vallone, C.A.; Greengard, J.S.; Crabtre
Proc. Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985
A:Title: A viral long terminal repeat in the interleukin 2 gene of a cell line that c
A:Reference number: A94067; MUID:86042650; PMID:3877307
A:Accession: A94067
A:Molecule type: mRNA
A:Residues: 1-153 <CHE>
A:Cross-references: GB:M11144; NID:g177014; PIDN:AAA35454.1; PID:g177015
A:Experimental source: leukemia cell line M1A 144; ATCC TIB 201
A:Note: the integration of a retrovirus sequence containing a 5' LTR into the 3' nonc
C:Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-153/Product: interleukin-2 #status predicted <IL2>
F:23/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:78-125/Disulfide bonds: #status predicted
Query Match 93.0%; Score 147; DB 1; Length 153;
Best Local Similarity 96.8%; Pred. No. 7.4e-14;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 APTSSSTKKTQLEHLLKLQMLNGINNY 32
Db 21 APTSSSTKKTQLEHLLKLQMLNGINNY 51
RESULT 3
JN0698
interleukin 2 precursor - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999
C:Accession: JN0698
R:Cozzi, P.J.; Padrid, P.A.; Takeda, J.; Alegrre, M.L.; Yuhkl, N.; Leff, A.R.
Biochem. Biophys. Res. Commun. 194, 1038-1043, 1993
A:Title: Sequence and functional characterization of feline interleukin 2.
A:Reference number: JN0698; MUID:93356765; PMID:8352761

A:Accession: JN0698
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-154 <COZ>
A:Cross-references: GB:L19402; NID:g304313; PIDN:AAA02865.1; PID:g304314
C:Superfamily: interleukin-2
C:Keywords: growth factor

Query Match 67.7%; Score 107; DB 2; Length 154;
Best Local Similarity 70.0%; Pred. No. 4.5e-08;
Matches 21; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLMILNGINNY 31
||||| : ||| ||| : ||| : ||| : |||
Db 21 APASSSTKRETKQLEQLLDLKLNGVNN 50

RESULT 4
A31278
interleukin-2 precursor - rat
N:Alternate names: IL-2; T-cell growth factor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Apr-1989 #sequence_revision 26-Apr-1989 #text_change 16-Jul-1999
C:Accession: A45882; A31278
R:McKnight, A.J.; Mason, D.W.; Barclay, A.N.
Immunogenetics 30, 145-147, 1989
A:Title: Sequence of rat interleukin 2 and anomalous binding of a mouse interleukin 2 cDNA
A:Reference number: A45882; MUID:89339608; PMID:2788130
A:Accession: A45882
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <MCK>
A:Cross-references: GB:M22899; NID:g204909; PIDN:AAA41427.1; PID:g204910
C:Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell

Query Match 61.4%; Score 97; DB 2; Length 155;
Best Local Similarity 64.5%; Pred. No. 1.3e-06;
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLMILNGINNY 32
||||| : ||| ||| : ||| : ||| : |||
Db 21 APTSSPAKETQHQLEQLLDLQVLLRGIDNY 51

RESULT 5
S16241
interleukin-2 precursor - pig
N:Alternate names: IL-2; T-cell growth factor
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C:Accession: S16241; S15473
R:Goodall, J.C.; Emery, D.C.; Bailey, M.; English, L.S.; Hall, L.
Biochim. Biophys. Acta 1089, 257-258, 1991
A:Title: cDNA cloning of porcine interleukin 2 by polymerase chain reaction.
A:Reference number: S16241; MUID:91274360; PMID:2054386
A:Accession: S16241
A:Molecule type: mRNA
A:Residues: 1-154 <GOO>
A:Cross-references: EMBL:X56750; NID:g1991; PIDN:CAA40071.1; PID:g1992
R:Lefevre, F.
submitted to the EMBL Data Library, March 1991
A:Description: Molecular cloning of porcine interleukin 2 cDNA by the polymerase chain reaction
A:Reference number: S15473
A:Accession: S15473
A:Molecule type: mRNA
A:Residues: 1-154 <LEF>
A:Cross-references: EMBL:X58428; NID:g2068; PIDN:CAA41330.1; PID:g2069
C:Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-154/Product: interleukin-2 #status predicted <MAT>

Query Match 60.8%; Score 96; DB 2; Length 154;
Best Local Similarity 64.5%; Pred. No. 1.7e-06;
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLMILNGINNY 32
||||| : ||| ||| : ||| : ||| : |||
Db 21 APTSSSTKKTQLEPLLDLQLLKEVKNY 51

RESULT 6
S33509
interleukin-2 - Mongolian jird
C:Species: Meriones unguiculatus (Mongolian jird)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C:Accession: S33509
R:Mai, Z.; Klei, T.; Horohov, D.
submitted to the EMBL Data Library, October 1992
A:Description: Cross-species PCR cloning of Jird (Meriones unguiculatus) interleukin-2
A:Reference number: S33509
A:Accession: S33509
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <MAI>
A:Cross-references: EMBL:X68779; NID:g577588; PIDN:CAA48679.1; PID:g311638
C:Superfamily: interleukin-2

Query Match 60.1%; Score 95; DB 2; Length 155;
Best Local Similarity 64.5%; Pred. No. 2.5e-06;
Matches 20; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLMILNGINNY 32
||||| : ||| ||| : ||| : ||| : |||
Db 21 APTSSPAKQAQYQLQLLDLQQLLRGINNY 51

RESULT 7
S31391
interleukin-2 precursor - horse
C:Species: Equus caballus (domestic horse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S31391
R:Tavernor, A.S.; Butcher, G.W.
submitted to the EMBL Data Library, November 1992
A:Description: cDNA cloning of equine interleukin-2 by polymerase chain reaction.
A:Reference number: S31391
A:Accession: S31391
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-149 <TAV>
A:Cross-references: EMBL:X69393; NID:g1076; PIDN:CAA49190.1; PID:g1077
C:Superfamily: interleukin-2

Query Match 53.8%; Score 85; DB 2; Length 149;
Best Local Similarity 53.3%; Pred. No. 6.5e-05;
Matches 16; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLMILNGINNY 31
||||| : ||| ||| : ||| : ||| : |||
Db 21 APTSSSKRETQKQKQLQMDLKLLEGVNN 50

RESULT 8
S38662
interleukin-2 - goat
C:Species: Capra aegagrus hircus (domestic goat)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C:Accession: S38662
R:Rimstad, E.
submitted to the EMBL Data Library, November 1993
A:Description: The molecular cloning and expression of caprine interleukin 2.
A:Reference number: S38662
A:Accession: S38662
A:Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-155 <RI
A;Cross-references: E
C;Superfamily: interl

Query Match 45.6%; Score 72; DB 2; Length 155;
Best Local Similarity 50.0%; Pred. NO. 0.0052;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 2 APTSSSTKKTQLQLEHLLKLQMLNGINN 31
 ||||| | :: ||| ||:| : |
 Db 21 APTSSSTGNTMKEVKSLLLDLQLLEKVKN 50

RESULT 9

S11488
interleukin-2 precursor - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S11488; S13102; S13517
R:Goodall, J.C.; Emery, D.C.; Perry, A.C.F.; English, L.S.; Hall, L.
Nucleic Acids Res. 18, 5883, 1990
A:Title: cDNA cloning of ovine interleukin 2 by PCR.
A:Reference number: S11488; MUID:91016933; PMID:2216781

A:Accession: S11488
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <GOO>
A:Cross-references: EMBL:X53934; NID:g1281; PIDN:CAA37881.1; PID:g1282
R:Seow, H.F.; Rochet, J.S.; Radford, A.J.; Wood, P.R.
Nucleic Acids Res. 18, 7175, 1990
A:Title: The molecular cloning of ovine interleukin 2 gene by the polymerase chain reaction
A:Reference number: S13102; MUID:91088336; PMID:2363496

Query Match 45.6%; Score 72; DB 2; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.0052;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

```
QY 2 APTSSSTKKTQLQLEHLLKLQMLNGINN 31
      ||||| | :: ||| ||::| |
Db 21 APTSSSTGNTNMKEVKSLLLOLQLEKVK 50
```

RESULT 10
I45913

interleukin-2 precursor - bovine

C.Species: Bos primigenius taurus (cattle)
C.Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C.Accession: I45913; S21470; S20761
R.Cerretti, D.P.; McKerrehgan, K.; Larsen, A.; Cantrell, M.A.; Anderson, D.; Gillis, S.;
Proc. Natl. Acad. Sci. U.S.A. 83, 3223-3227, 1986
A.Title: Cloning, sequence, and expression of bovine interleukin 2.
A.Reference number: I45913; MUID:86205869; PMID:3517854
A.Accession: I45913

submitted to the EMBL Data Library, December 1989
A; Reference number: S21470

A;Accession: S21470
A;Molecule type: DNA
A;Residues: 1-22 <AN2>
A;Cross-references: EMBL:X17201; NID:g452; PIDN:CAA35062.1; PID:g453
C;Genetics:
A;Gene: IL-2

Query Match 45.6%; Score 72; DB 2; Length 155;
Best Local Similarity 50.0%; Pred. NO. 0.0052;
Matches 15; Conservative 6; Mismatches 9; Indels

Qy 2 APTSSSTKKTQLOLEHLLLLKLQMLNGINN 31
 ||||| | : : ||| ||: | : |
 Db 21 APTSSSTGNTMKEVKSLDDLQLLLEKVKVN 50

RESULT 11
S37289

interleukin-2 precursor - mouse

C; Species: Mus musculus (house mouse)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C; Accession: S37289; S27205; S36162; S24936
R; Todd, J.A.

submitted to the EMBL Data Library, April 1993

A:Reference number: S37289

A:Accession: S37289

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-169 <TOD>

A:Cross-references: EMBL:X73040

B:Watesanz, F.; Alcina, A.; Pellicer, A.
Biochim. Biophys. Acta 1132, 335-336, 1992

A:Title: A new cDNA sequence for the murine Interleukin-2 gene.

A:Reference number: S27205; MUID:93041941; PMID:1420317

Query Match 43.7%; Score 69; DB 2; Length 169;
Best Local Similarity 45.9%; Pred. No. 0.015;
Matches 17; Conservative 6; Mismatches 8; Indels

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QY 2 APTSSSTKKTLQ-----LEHLLLLKLQMLNGINNY 32
      :||||| : | | | | | | | | | | : | |
Db 29 SPTSSSTAEEAQOQQOQQOQHLEOLLMDLOELLSMENY 65
```

RESULT 12
ICMS2

interleukin-2 precursor - mouse

N:Alternate names: IL-2, T-cell growth factor (TCGF)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jul-2000
 C:Accession: A54490; A54490; A94064; I48570; A01850; I84713
 R:Fuse, A.; Fujita, T.; Yasumitsu, H.; Kashima, N.; Hasedawa, K.; Taniguchi, T.

Best Local Similarity 37.9%; Pred. No. 0.25;
Matches 11; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 4 TSSSTKKTQLQHLLKLQMLNGINNY 32
||||| :||: ||: ||: ||: ||: ||: ||:
DB 22 SSSSVLEIVLDEIITKLNLISEINNY 50

RESULT 14
GNLJG4
HIV-1 retropepsin (EC 3.4.23.16) - simian immunodeficiency virus (African green monkey)
N:Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA P
C:Species: simian immunodeficiency virus, SIV
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 03-Jun-2002
C:Accession: B30045
R:Fukasawa, M.; Miura, T.; Hasegawa, A.; Morikawa, H.; Tsujimoto, H.; Mikit, K.; Kitam
Nature 333, 457-461, 1988
A:Title: Sequence of simian immunodeficiency virus from African green monkey, a new m
A:Reference number: A30045; MUID:88232906; PMID:3374586
A:Accession: B30045
A:Molecule type: DNA
A:Residues: 1-1061 <PUK>
A:Cross-references: EMBL:X07805; NID:g61748; PID:gl335593
C:Comment: Specific enzymatic cleavages may yield mature proteins including protease,
C:Genetics:
A:Gene: pol
C:Superfamily: pol polyprotein
C:Keywords: aspartic proteinase; hydrolase; nucleotidyltransferase; polyprotein; reve
F:l1l-2l0/Product: retropepsin #status predicted <RP>
F:l34/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 34.2%; Score 54; DB 1; Length 1061;
Best Local Similarity 58.8%; Pred. No. 17;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 11 TQLOEHLHLKLQMLNLN 27
||||| :||: ||: ||: ||: ||: ||: ||:
DB 976 TQLEIQHLQTKIKILN 992

RESULT 15
SL2169
Isopenicillin N acyltransferase (EC 2.3.1.-) - Emericella nidulans
N:Alternate names: acyl coenzyme A-6-aminopenicillanic acid acyltransferase; acylan
C:Species: Emericella nidulans, Aspergillus nidulans
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: SL2169; A36142; S09090
R:Montenegro, E.; Barredo, J.L.; Gutierrez, S.; Diez, B.; Alvarez, E.; Martin, J.F.
Mol. Gen. Genet. 221, 322-330, 1990
A:Title: Cloning, characterization of the acyl-CoA:6-amino penicillanic acid acylan
A:Reference number: SL2169; MUID:90340281; PMID:2166227
A:Accession: SL2169
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <MON>
A:Cross-references: EMBL:X53310; NID:g2378; PIDN:CAA37394.1; PID:g2379
R:Tobin, M.B.; Fleming, M.D.; Skatrud, P.L.; Miller, J.R.
J. Bacteriol. 172, 5908-5914, 1990
A:Title: Molecular characterization of the acyl-coenzyme A:isopenicillin N acylan
herichia coli.
A:Reference number: A36142; MUID:91008967; PMID:2120195
A:Accession: A36142
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <TOB>
A:Cross-references: GB:M58293; NID:g167999; PIDN:AAA33287.1; PID:g168000
R:Whiteman, P.A.; Abraham, E.P.; Baldwin, J.E.; Fleming, M.D.; Schofield, C.J.; Suthe
FEBS Lett. 262, 342-344, 1990
A:Title: Acyl coenzyme A: 6-aminopenicillanic acid acyltransferase from Penicillium c
A:Reference number: S09089; MUID:90242961; PMID:2110531
A:Accession: S09090
A:Molecule type: protein
A:Residues: 103-122 <WHI>

A: Molecule type: protein
A: Residues: 103-122 <WHI>

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C:Genetics:
A:Introns: 12/3; 71/1; 121/3
C:Keywords: acyltransferase

Query Match      33.5%;      Score 53;  DB 2;  Length 357;
Best Local Similarity 52.6%;  Pred. No. 7.2;
Matches 10;  Conservative 5;  Mismatches 4;  Indels 0;  Gaps 0;

Qy      8  TKKTQLQLEHLLKLQML 26
      ||||| :| | | :| :|
Db      40  TKKTQAEQLLRELEQVM 58

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Search completed: November 22, 2002, 13:13:26
Job time : 16 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 13:11:55 ; Search time 10 Seconds
(without alignments)
50.117 Million cell updates/sec

Title: US-09-776-781-6

Perfect score: 158

Sequence: 1 MAPSSSTKKTQLEHLLKLQMLINGINNY 32

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	149	94.3	381	10	US-09-822-698A-5
2	147	93.0	133	9	US-10-051-657A-1
3	147	93.0	133	10	US-09-766-543-8
4	147	93.0	153	10	US-09-149-721-3
5	147	93.0	153	10	US-09-923-246-111
6	143	90.5	133	10	US-09-766-543-14
7	143	90.5	331	10	US-09-033-525-2
8	57	36.1	43	10	US-09-835-147-11
9	57	36.1	454	10	US-09-835-147-6
10	57	36.1	478	10	US-09-835-147-8
11	57	36.1	487	10	US-09-835-147-26
12	51	32.3	751	10	US-09-881-752A-280
13	51	32.3	866	10	US-09-815-242-11373
14	50	31.6	37	9	US-10-142-120-1
15	47	29.7	226	10	US-09-796-149-5
16	47	29.7	515	10	US-09-925-300-1285
17	46	29.1	1403	9	US-10-108-605-93
18	44	27.8	284	10	US-09-810-997-1
19	44	27.8	1230	10	US-09-881-752A-150

20	43.5	27.5	84	10	US-09-864-761-36104	Sequence 36104, A
21	43.5	27.5	908	10	US-09-895-072-15	Sequence 15, Appl
22	43.5	27.5	908	10	US-09-896-552-15	Sequence 15, Appl
23	43.5	27.5	928	10	US-09-895-072-1	Sequence 1, Appli
24	43.5	27.5	928	10	US-09-896-552-1	Sequence 1, Appli
25	43	27.2	248	10	US-09-848-294-10	Sequence 10, Appl
26	43	27.2	309	10	US-09-788-626-12	Sequence 12, Appl
27	43	27.2	421	10	US-09-841-132-577	Sequence 577, App
28	43	27.2	473	10	US-09-835-147-29	Sequence 29, Appl
29	43	27.2	990	12	US-10-047-676A-7	Sequence 7, Appli
30	43	27.2	1034	10	US-09-815-242-10331	Sequence 10331, A
31	42.5	26.9	1145	9	US-09-866-557A-5	Sequence 5, Appli
32	42	26.6	45	10	US-09-864-761-43127	Sequence 43127, A
33	42	26.6	214	10	US-09-925-300-1589	Sequence 1589, Ap
34	42	26.6	529	10	US-09-815-242-13935	Sequence 13935, A
35	42	26.6	964	10	US-09-841-132-177	Sequence 177, App
36	42	26.6	977	10	US-09-841-132-191	Sequence 191, App
37	42	26.6	1049	10	US-09-815-242-10072	Sequence 10072, A
38	42	26.6	1049	10	US-09-815-242-13719	Sequence 13719, A
39	41.5	26.3	65	10	US-09-784-869-999	Sequence 999, App
40	41.5	26.3	267	10	US-09-815-242-11549	Sequence 11549, A
41	41	25.9	41	10	US-09-815-242-10672	Sequence 10672, A
42	41	25.9	71	10	US-09-864-761-35411	Sequence 35411, A
43	41	25.9	110	10	US-09-815-242-5029	Sequence 5029, Ap
44	41	25.9	172	10	US-09-864-761-40611	Sequence 40611, A
45	41	25.9	338	10	US-09-841-805A-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-822-698A-5

; Sequence 5, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft word

; SEQ ID NO 5

; LENGTH: 381

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: MUC1-specific immunocytokine biVPH1-IL-2

US-09-822-698A-5

Query Match 94.3%; Score 149; DB 10; Length 381;

Best Local Similarity 93.8%; Pred. No. 6e-15;

Matches 30; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTQLEHLLKLQMLINGINNY 32

Db 248 LAPSSSTKKTQLEHLLKLQMLINGINNY 279

RESULT 2

US-10-051-657A-1

; Sequence 1, Application US/10051657A

; Patent No. US20020164300A1

; GENERAL INFORMATION:

; APPLICANT: Chan, Sham-Yuen

; APPLICANT: Kelly, Ruth

; TITLE OF INVENTION: Interleukin-2 Mutein Expressed from Mammalian Cells

; FILE REFERENCE: MSB-7257

; CURRENT APPLICATION NUMBER: US/10/051,657A

; CURRENT FILING DATE: 2002-04-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-051-657A-1

Query Match 93.0%; Score 147; DB 9; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.4e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLMILNGINNY 32
|||||
Db 1 APTSSSTKKTQLEHLLKQLMILNGINNY 31

RESULT 3
US-09-766-543-8
; Sequence 8, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human IL-2
US-09-766-543-8

Query Match 93.0%; Score 147; DB 10; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.4e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLMILNGINNY 32
|||||
Db 1 APTSSSTKKTQLEHLLKQLMILNGINNY 31

RESULT 4
US-09-149-721-3
; Sequence 3, Application US/09149721
; Patent No. US20020058799A1
; GENERAL INFORMATION:
; APPLICANT: Mumper, Russ; Tagliaferri, Frank
; TITLE OF INVENTION: HYDROPHOBIC GLYCOSYLAMINE DERIVATIVES, COMPOSITIONS, AND METHODS
; FILE REFERENCE: 237/023
; CURRENT APPLICATION NUMBER: US/09/149,721
; CURRENT FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 60/058,259
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of human IL-2
US-09-149-721-3

Query Match 93.0%; Score 147; DB 10; Length 153;
Best Local Similarity 96.8%; Pred. No. 4e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLMILNGINNY 32
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Db 21 APTSSSTKKTQLEHLLKQLMILNGINNY 51

RESULT 5
US-09-923-246-111
; Sequence 111, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald D.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-111

Query Match 93.0%; Score 147; DB 10; Length 153;
Best Local Similarity 96.8%; Pred. No. 4e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLMILNGINNY 32
|||||
Db 21 APTSSSTKKTQLEHLLKQLMILNGINNY 51

RESULT 6
US-09-766-543-14
; Sequence 14, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hIL-2

US-09-766-543-14

Query Match 90.5%; Score 143; DB 10; Length 133;
Best Local Similarity 96.7%; Pred. No. 1.4e-14;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PTSSSTKKTQLEHLLKLQMLNGINNY 32
Db 2 PTSSSTKKTQLEHLLKLQMLNGINNY 31

RESULT 7

US-09-033-525-2
; Sequence 2, Application US/09033525
; Patent No. US20020090374A1
; GENERAL INFORMATION:
; APPLICANT: Yarkoni, Shai
; APPLICANT: Ben-Yehudah, Ahmi
; APPLICANT: Azar, Yehudith
; APPLICANT: Aqelian, Rami
; APPLICANT: Belotstotsky, Ruth
; APPLICANT: Lorberboun-Galski, Haya
; TITLE OF INVENTION: CHIMERIC PROTEINS WITH CELL-TARGETING
; FILE REFERENCE: 9457-009-999
; CURRENT APPLICATION NUMBER: US/09/033,525
; CURRENT FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-033-525-2

Query Match 90.5%; Score 143; DB 10; Length 331;
Best Local Similarity 96.7%; Pred. No. 4e-14; Length 331;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PTSSSTKKTQLEHLLKLQMLNGINNY 32
Db 4 PTSSSTKKTQLEHLLKLQMLNGINNY 33

RESULT 8

US-09-835-147-11
; Sequence 11, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion

; OTHER INFORMATION: construct of human CD39
US-09-835-147-11

Query Match 36.1%; Score 57; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQL 13
Db 25 APTSSSTKKTQL 36

RESULT 9

US-09-835-147-6
; Sequence 6, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-6

Query Match 36.1%; Score 57; DB 10; Length 454;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQL 13
Db 1 APTSSSTKKTQL 12

RESULT 10

US-09-835-147-8
; Sequence 8, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955


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RESULT 14
US-10-142-120-1
; Sequence 1, Application US/10142120
; Patent No. US20020164302A1
; GENERAL INFORMATION:
; APPLICANT: Epstein, Alan L.
; TITLE OF INVENTION: VASOPERMABILITY ENHANCING PEPTIDE FRAGMENT OF HUMAN INTERLEUKIN-
; FILE REFERENCE: 1920-325D2-09801297
; CURRENT APPLICATION NUMBER: US/10/142,120
; CURRENT FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 09/443,061
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 08/806,121
; PRIOR FILING DATE: 1996-12-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-142-120-1
Query Match 31.6%; Score 50; DB 9; Length 37;
Best Local Similarity 90.0%; Pred. No. 0.26;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 23 OMILINGINNY 32
DB 1 EMILINGINNY 10

RESULT 15
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; Sequence 5, Application US/09796149
; Patent No. US20020035079A1
; GENERAL INFORMATION:
; APPLICANT: Univ. of Southern California
; TITLE OF INVENTION: Mutated cyclin G1 protein
; FILE REFERENCE: 4-31342A/USC
; CURRENT APPLICATION NUMBER: US/09/796,149
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-149-5
Query Match 29.7%; Score 47; DB 10; Length 226;
Best Local Similarity 60.0%; Pred. No. 6.4;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 8 TTKTQLQLEHLHLKL 22
DB 82 TRQVLRMEHLVLKV 96

Search completed: November 22, 2002, 13:14:04
Job time : 11 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 13:11:34 ; Search time 14 Seconds
(without alignments)
67.252 Million cell updates/sec

Title: US-09-776-781-6
Perfect score: 158
Sequence: 1 MAPTSSSRKTKQLQLHLLKLQMLGINNY 32

Scoring table: BLOSUM62
Gap10 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	147	93.0	50	1	US-08-127-351-13
5	147	93.0	50	1	US-08-480-367B-13
6	147	93.0	50	1	US-08-487-221A-13
7	147	93.0	50	1	US-08-480-370-13
8	147	93.0	88	4	US-08-817-787-15
9	147	93.0	133	1	US-07-800-366-1
10	147	93.0	133	1	US-08-354-456A-5
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12	147	93.0	133	1	US-08-318-193-89
13	147	93.0	133	1	US-08-284-393B-1
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15	147	93.0	133	1	US-08-284-393B-3
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17	147	93.0	133	3	US-08-722-258-3
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22	147	93.0	133	5	PCT-US95-08950-2
23	147	93.0	133	5	PCT-US95-08950-3
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25	147	93.0	133	6	5256769-1
26	147	93.0	133	6	5464939-2
27	147	93.0	153	3	US-09-012-366-3

28	147	93.0	153	4	US-08-759-628-8	Sequence 8, Appli
29	147	93.0	153	4	US-09-522-217-111	Sequence 111, App
30	147	93.0	153	6	5314995-7	Patent No. 5314995
31	147	93.0	157	4	US-08-818-562-2	Sequence 2, Appli
32	147	93.0	157	4	US-09-628-445-2	Sequence 2, Appli
33	147	93.0	478	3	US-08-155-888-2	Sequence 2, Appli
34	147	93.0	504	1	US-07-932-915-2	Sequence 2, Appli
35	147	93.0	504	5	PCT-US91-05826-2	Sequence 2, Appli
36	145	91.8	31	4	US-09-116-594-2	Sequence 2, Appli
37	144	91.1	251	3	US-08-875-811-59	Sequence 59, Appl
38	144	91.1	254	3	US-08-875-811-61	Sequence 61, Appl
39	143	90.5	133	1	US-08-354-456A-6	Sequence 6, Appli
40	132.5	83.9	127	3	US-08-806-121B-3	Sequence 3, Appli
41	132.5	83.9	127	4	US-09-443-061-3	Sequence 3, Appli
42	100	63.3	141	4	US-08-930-917A-18	Sequence 18, Appl
43	96	60.8	21	4	US-09-570-921-63	Sequence 63, Appl
44	96	60.8	21	4	US-09-570-921-68	Sequence 68, Appl
45	72	45.6	135	2	US-08-383-621-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-160-376A-5
; Sequence 5, Application US/08160376A
; Patent No. 5473049
; GENERAL INFORMATION:
; APPLICANT: Obermeier, Ranier
; APPLICANT: Gerl, Martin
; APPLICANT: Ludwig, Jurgen
; APPLICANT: Sabel, Walter
; TITLE OF INVENTION: Process For Obtaining Proinsulin
; TITLE OF INVENTION: Possessing Correctly Linked
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth A. Genoni, Esq.
; STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500
; CITY: Somerville
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08876-1258
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 386
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/160,376A
; FILING DATE: December 1, 1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GE P 4240420.7
; FILING DATE: December 2, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara V. Maurer, Esq.
; REGISTRATION NUMBER: 31,287
; REFERENCE/DOCKET NUMBER: HOE 92/F 384
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 231-4079
; TELEFAX: (908) 231-2255
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 Amino Acids
; TYPE: Amino Acid (AA)
; TOPOLOGY: not relevant
; US-08-160-376A-5

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Best Local Similarity 96.9%; Pred. No. 4.1e-16;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

; Sequence 13, Application US/08480367B
; Patent No. 5578288
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: 2654-002A
; APPLICATION NUMBER: US/08/480.367B
; FILING DATE: 07-06-95
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-480-367B-13

Query Match 93.0%; Score 147; DB 1; Length 50;
Best Local Similarity 96.8%; Pred. No. 1.1e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0;

QY 2 APTSSSTKKTQLEHLLKLQMLINGINNY 32
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Db 1 APTSSSTKKTQLEHLLKLQMLINGINNY 31
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RESULT 6
US-08-487-221A-13
; Sequence 13, Application US/08487221A
; Patent No. 5591656
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESS: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/08/487,221A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-487-221A-13

Query Match 93.0%; Score 147; DB 1; Length 50;
Best Local Similarity 96.8%; Pred. No. 1.1e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0;

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Db 1 APTSSSTKKTQLEHLLKLQMLINGINNY 31
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RESULT 7
US-08-480-370-13
; Sequence 13, Application US/08480370
; Patent No. 5609847
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESS: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/480,370
; APPLICATION NUMBER: US/08/480,370
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-480-370-13

Query Match 93.0%; Score 147; DB 1; Length 50;
Best Local Similarity 96.8%; Pred. No. 1.1e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 APTSSSTKKTQLEHLLKQMLNGINNY 31

RESULT 8

US-08-817-787-15
; Sequence 15, Application US/08817787
; Patent No. 6294353
; GENERAL INFORMATION:
; APPLICANT: Pack, Peter
; APPLICANT: Lupas, Andrei
; TITLE OF INVENTION: TARGETED HETERO-ASSOCIATION OF
; NUMBER OF INVENTIONS: RECOMBINANT PROTEINS TO MULTI-FUNCTIONAL COMPLEXES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020

COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/08/817,787
; FILING DATE: 23-SEP-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04117
; FILING DATE:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94 11 6558.1
; FILING DATE: 20-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090

; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 88 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-817-787-15

Query Match 93.0%; Score 147; DB 4; Length 88;
Best Local Similarity 96.8%; Pred. No. 2.2e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 3 APTSSSTKKTQLEHLLKQMLNGINNY 33

RESULT 9

US-07-800-366-1
; Sequence 1, Application US/07800366
; Patent No. 5250296
; GENERAL INFORMATION:
; APPLICANT: OOTSU, Koichiro
; TITLE OF INVENTION: IMMUNOSTIMULANT AGENT CONTAINING
; INTERLEUKIN-2 AND 5'-DEOXY-5-FLUOROURIDINE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/800,366
; FILING DATE: 19911127
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Castle, Donald R
; REGISTRATION NUMBER: 24,220
; REFERENCE/DOCKET NUMBER: 41417(281)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-800-366-1

Query Match 93.0%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
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DB 1 APTSSSTKKTQLEHLLKQMLNGINNY 31

RESULT 10

US-08-354-456A-5
; Sequence 5, Application US/08354456A
; Patent No. 5567611
; GENERAL INFORMATION:
; APPLICANT: Ralph, Peter
; APPLICANT: Martin, George
; APPLICANT: Platek, Michael
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: Multifunctional M-CSF Proteins and Genes Encoding
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: Intellectual Property - R440, P.O. Box 8097
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94662-8097


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: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/284,393B
: FILING DATE: 01-AUG-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Ching, Edwin P.
: REGISTRATION NUMBER: 34,090
: REFERENCE/DOCKET NUMBER: DX0389
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-852-9196
: TELEFAX: 415-496-1200
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 133 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-284-393B-2

Query Match 93.0%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels

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Db 1 APTSSSTKKTQLQLEHLLKLQMLNGINNY 31

RESULT 15
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: Sequence 3, Application US/08284393B
: Patent No. 5696234
: GENERAL INFORMATION:
: APPLICANT: Zurawski, Sandra M.
: TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DNAX Research Institute
: STREET: 901 California Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/284,393B
: FILING DATE: 01-AUG-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Ching, Edwin P.
: REGISTRATION NUMBER: 34,090
: REFERENCE/DOCKET NUMBER: DX0389
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-852-9196
: TELEFAX: 415-496-1200
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 133 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-284-393B-3

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Query Match 93.0%; Score 147; DB 1; Length 133;
 Best Local Similarity 96.8%; Pred. No. 3.6e-15;
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Search completed: November 22, 2002, 13:13:47
 Job time : 15 secs

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Total number of hits satisfying chosen parameters: 908470
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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
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2	154	97.5	134 8 AAB70573 Sequence of segmen
3	153	96.8	31 23 ABB79535 Interleukin-2 pept
4	153	96.8	133 21 AAY53825 Amino acid sequenc
5	152	96.2	58 12 AAR11015 Human interleukin-
6	152	96.2	60 11 AAR06838 Human IL-2 N-termi
7	152	96.2	60 15 AAR48245 Human Interleukin-
8	152	96.2	96 15 AAR68899 Human pro-insulin
9	152	96.2	96 16 AAR78662 Fusion protein con
10	152	96.2	133 13 AAR22595 Interleukin-2 used

11	152	96.2	134 5 AAP40050 Sequence of an int
12	152	96.2	134 6 AAP50053 Sequence I of new
13	152	96.2	134 6 AAP50855 Sequence encoded b
14	152	96.2	134 7 AAP61102 Sequence of mature
15	152	96.2	134 8 AAP70585 Sequence of human
16	152	96.2	134 11 AAR05267 Sequence of natura
17	152	96.2	134 11 AAR05266 Sequence of natura
18	152	96.2	134 11 AAR05240 Sequence of natura
19	152	96.2	136 20 AAY49917 Human interleukin
20	152	96.2	143 15 AAR50932 tabl. Synthetic.
21	152	96.2	149 11 AAR07265 Recombinant Interl
22	152	96.2	149 11 AAR07266 Recombinant Interl
23	152	96.2	149 11 AAR07267 Recombinant Interl
24	152	96.2	149 11 AAR07269 Recombinant Interl
25	152	96.2	149 11 AAR07148 Recombinant Interl
26	152	96.2	149 11 AAR07149 Recombinant Interl
27	152	96.2	149 11 AAR07150 Recombinant Interl
28	152	96.2	149 11 AAR07261 Recombinant Interl
29	152	96.2	149 11 AAR07262 Recombinant Interl
30	152	96.2	149 11 AAR07263 Recombinant Interl
31	152	96.2	149 11 AAR07264 Recombinant Interl
32	152	96.2	172 10 AAP94809 Human interleukin
33	152	96.2	201 11 AAR06839 Human IL-2 N-termi
34	152	96.2	255 6 AAP50305 Fused antibody inter
35	152	96.2	273 6 AAP50087 Conjugate of inter
36	152	96.2	273 6 AAP50310 Interferon-gamma a
37	150	94.9	133 21 AAY53829 Amino acid sequenc
38	149	94.3	65 10 AAP91032 Human interleukin-
39	149	94.3	133 21 AAY53828 Amino acid sequenc
40	149	94.3	149 11 AAR07146 Recombinant Interl
41	149	94.3	149 11 AAR07268 Recombinant Interl
42	149	94.3	149 11 AAR07255 Recombinant Interl
43	149	94.3	149 11 AAR07256 Recombinant Interl
44	149	94.3	149 11 AAR07257 Recombinant Interl
45	149	94.3	149 11 AAR07258 Recombinant Interl

ALIGNMENTS

RESULT 1			
AB79534	AB79534	standard; Peptide; 32 AA.	
ID	AB79534	standard; Peptide; 32 AA.	
XX	AB79534		
AC	AB79534		
XX			
DT	23-SEP-2002	(first entry)	
XX			
DE	Interleukin-2 peptide IP131 (D20K).		
XX			
KW	IP131; interleukin-2; human; gene; gene therapy; mutant; mutein.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference 21		
FT	/note= "wild-type Asp substituted by Lys"		
XX			
PN	US2002044935-A1.		
XX			
PD	18-APR-2002.		
XX			
PF	06-FEB-2001; 2001US-0776781.		
XX			
PR	16-JUL-1998; 98US-0116594.		
PR	12-SEP-2000; 2000US-0660465.		
XX			
PA	(INSP) INST PASTEUR.		
XX			
PI	Theze J, Eckenberg R, Moreau J, Goldberg M, Rose T, Alzari P;		
PI	Mazie J;		
XX			

DR WPI: 2002-546505/58.
DR N-PSDB; ABN84295.
XX
PT New peptides derived from Interleukin 2 designated IP130 and IP131 are
PT useful as therapeutic agents in the treatment of patients deficient in
PT IL-2 activity -
XX
XX
PS Claim 18; Page 2; 53pp; English.
XX
XX The present sequence is the protein sequence for IP131 D20K. The
CC sequence is based on the human interleukin-2 (IL-2) peptide IP130
CC (see ABN84292) by the addition of a C-terminal Tyr residue, and
CC substitution of the native Asp-20 residue by Lys. Asp-20 is
CC located in a region of IL-2 that directly influences interaction of
CC the cytokine with its receptor (IL-2R). An antibody that binds to
CC the peptide is claimed, and is preferably an antibody produced by
CC hybridoma H2-8 (CNCM No. I-2338). A claimed method of detecting
CC the presence or activity of involves contacting a sample with
CC IP131 D20K, and detecting whether binding occurs. A claimed method
CC for inhibiting IL-2R activity involves contacting IL-2R with the
CC peptide. A claimed method for inducing IL-2 activity in a patient
CC comprises administering IP131 D20K to the patient. A vector
CC containing DNA encoding the peptide is claimed, and is used in a
CC claimed method for treating a patient deficient in IL-2 activity.
CC Also claimed are peptides corresponding to IP131 D20K but
CC containing conservative amino acid substitutions, i.e. change of
CC non-polar R-groups but other non-polar R-groups, change of
CC uncharged polar R-groups by other uncharged polar R-groups,
CC substitution of Arg by Lys, Asp by Glu, Thr by Ser, or Asn by
CC Gln, and vice versa. The peptide induces SHC phosphorylation or
CC induction of the SHC/WAPK pathway. Antibodies specific for the
CC peptide are useful for treatment or prevention of undesirable
CC immune reactions such as graft rejection, or autoimmune disorders
CC such as rheumatoid arthritis.
XX
XX
SQ Sequence 32 AA;

Query Match 100.0%; Score 158; DB 23; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPTSSSTKKTQLEHLLKQLMILNGINNY 32
Db 1 MAPTSSSTKKTQLEHLLKQLMILNGINNY 32

RESULT 2
AAP70573
XX AAP70573 standard; Protein; 134 AA.
XX
XX AAP70573;
XX
XX 27-MAY-1991 (first entry)
XX
XX Sequence of segments A-F of interleukin-2 (IL-2).
XX Interleukin-2 fusion protein; ballast fragment.
XX DE3636903-A.
XX
XX 02-JUL-1987.
XX
XX 30-OCT-1986; 86DE-3636903.
XX
XX 21-DEC-1985; 85DE-3545565.
XX
XX 30-OCT-1986; 86DE-3636903.
XX
XX (FARH) HOECHST AG.
XX
XX Habermann P;
XX
XX WPI: 1987-186353/27.
DR N-PSDB; AAN70921.

XX
PT New fusion protein contg. small interleukin 2 ballast fragments -
PT allowing control of product solubility, and corresp. genes,
XX vectors and transformed host cells
XX
PS Disclosure; pp8-9; 22pp; German.
XX
XX The inventors claim a novel fusion protein which has a C- or N-
CC terminal portion corresponding essentially to the AA sequence of
CC interleukin-2 (IL-2) but contg. less than 100 AAs. The IL-2 sequence
CC is coded for by 1.2 or 3 of the A-F segments of the IL-2 gene having
CC the formula: (EcoRI)-A-PstI-B-MinI-C-XbaI-D-SacI-E-PvuII-F-(Sall),
CC for example, the sequence in AAN70921. The segments are joined in any
CC appropriate sequence and opt. connected by usual adaptors or linkers.
XX
SQ Sequence 134 AA;

Query Match 97.5%; Score 154; DB 8; Length 134;
Best Local Similarity 96.9%; Pred. No. 4.7e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPTSSSTKKTQLEHLLKQLMILNGINNY 32
Db 1 MAPTSSSTKKTQLEHLLKQLMILNGINNY 32

RESULT 3
ABB79535
ID ABB79535 standard; Peptide; 31 AA.
XX
XX ABB79535;
AC ABB79535;
XX
XX 23-SEP-2002 (first entry)
DT
XX Interleukin-2 peptide IP131 (D20K).
XX
XX IP131; interleukin-2; human; gene; gene therapy; mutant; muten.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 20 /note= "wild-type Asp substituted by Lys"
FT
XX
XX US2002044935-A1.
XX
XX 18-APR-2002.
XX
XX 06-FEB-2001; 2001US-0776781.
XX
XX 16-JUL-1998; 98US-0116594.
XX
XX 12-SEP-2000; 2000US-0660465.
XX
XX (INSP) INST PASTEUR.
XX
XX Theze J, Eckenberg R, Moreau J, Goldberg M, Rose T, Alzari P;
PI Mazie J;
XX
XX WPI; 2002-546505/58.
DR N-PSDB; ABN84296.
XX
XX New peptides derived from Interleukin 2 designated IP130 and IP131 are
PT useful as therapeutic agents in the treatment of patients deficient in
PT IL-2 activity -
XX
XX Claim 18; Page -; 53pp; English.
XX
XX The present sequence is the protein sequence for IP131 D20K. The
CC sequence is based on the human interleukin-2 (IL-2) peptide IP130
CC (see ABN84292) by the addition of a C-terminal Tyr residue, and
CC substitution of the native Asp-20 residue by Lys. Asp-20 is
CC located in a region of IL-2 that directly influences interaction of
CC the cytokine with its receptor (IL-2R). An antibody that binds to
CC the peptide is claimed, and is preferably an antibody produced by
CC hybridoma H2-8 (CNCM No. I-2338). A claimed method of detecting
CC the presence or activity of involves contacting a sample with
CC IP131 D20K, and detecting whether binding occurs. A claimed method
CC for inhibiting IL-2R activity involves contacting IL-2R with the
CC peptide. A claimed method for inducing IL-2 activity in a patient
CC comprises administering IP131 D20K to the patient. A vector
CC containing DNA encoding the peptide is claimed, and is used in a
CC claimed method for treating a patient deficient in IL-2 activity.
CC Also claimed are peptides corresponding to IP131 D20K but
CC containing conservative amino acid substitutions, i.e. change of
CC non-polar R-groups but other non-polar R-groups, change of
CC uncharged polar R-groups by other uncharged polar R-groups,
CC substitution of Arg by Lys, Asp by Glu, Thr by Ser, or Asn by
CC Gln, and vice versa. The peptide induces SHC phosphorylation or
CC induction of the SHC/WAPK pathway. Antibodies specific for the
CC peptide are useful for treatment or prevention of undesirable
CC immune reactions such as graft rejection, or autoimmune disorders
CC such as rheumatoid arthritis.
XX
XX
SQ Sequence 32 AA;

Query Match 100.0%; Score 158; DB 23; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPTSSSTKKTQLEHLLKQLMILNGINNY 32
Db 1 MAPTSSSTKKTQLEHLLKQLMILNGINNY 32

RESULT 2
AAP70573
XX AAP70573 standard; Protein; 134 AA.
XX
XX AAP70573;
XX
XX 27-MAY-1991 (first entry)
XX
XX Sequence of segments A-F of interleukin-2 (IL-2).
XX Interleukin-2 fusion protein; ballast fragment.
XX DE3636903-A.
XX
XX 02-JUL-1987.
XX
XX 30-OCT-1986; 86DE-3636903.
XX
XX 21-DEC-1985; 85DE-3545565.
XX
XX 30-OCT-1986; 86DE-3636903.
XX
XX (FARH) HOECHST AG.
XX
XX Habermann P;
XX
XX WPI: 1987-186353/27.
DR N-PSDB; AAN70921.

Sequence 58 AA;

XX OS Homo sapiens.
XX PN ER2692594-A.

XX	24-DEC-1993.	92FR-0007571
PD		
XX		
PF	22-JUN-1992:	

PR 22-JUN-1992; 52ER-000/571
XX
PA (PERE/) PEREZ J.
XX

PI Perez J;
YY

DR WFL, 1954 020230/04:
DR N-PSDB: AA055629, AA

PT Application of optimised gene expression - for scientific.

PT industrial and therapeutic purposes
XX

PS disclosure; Fig 28 and Fig 29; 110pp; French.
XX

Resonances between coding and non-coding regions were measured for the native human IL-2 gene in plasmid pTg11 (see AAQ55630) and a synthetic IL-2 gene (AAQ35629) in which alternative, degenerate codons were used in order to introduce additional restriction sites. It was found that the degenerate changes greatly upset the "natural order" between coding and non-coding regions; as a result the amount of protein expressed by the degenerate gene is likely to be adversely affected. The inventors have proposed an "optimised" IL-2 gene with the aim of increasing the amount of protein expressed by the gene. (N.B. the sequence is also described as interleukin-6).

CC synthetic IL-2 gene (AAQ556)

XX
DE
CA-TAN-1080;

XX
BB
24 - TAN-1080.
9075-0012270

XX

[illegible]

DR N-PSDB; AAQ05976.

Query Match	96.2%	Score 152;	DB 15;	Length 60;
Best Local Similarity	96.9%	Pred. No. 3,8e-14;		

PS Disclosure; Fig 2; 11pp; Japanese.

QY	1	MAPTSSSTKKKTQLEHLLLDQMILNGINNY	32
Db	1	MAPTSSSTKKKTQLEHLLLDQMILNGINNY	32

Sequence 60 AA:

XX		
AC	AAR68899;	
XX		
DT	02-MAR-1995	(first entry)

XX	Human pro-insulin 2.
DE	
XX	
KW	Pro-insulin; A-chain; B-chain; C-chain; disulphide;
KW	mercaptan; chaotropic agent.

RESULT 7

AAR48245
ID AAR48245 standard: protein: 60 aa

XX
AC AAR48245.

XX

PF 25-NOV-1993; 93EP-0118993.
 XX
 PR 02-DEC-1992; 92DE-4240420.
 XX
 PA (FARH) HOECHST AG.
 XX
 PI Gerl M, Ludwig J, Obermeier R, Sabel W;
 XX
 XX WPI; 1994-177718/22.

XX Prodn. of pro-insulin with correct di.sulphide bridges - by
 PT treating recombinant precursor protein with mercaptan in alkali
 PT and in presence of chaotropic agent, then isolation on
 PT hydrophobic resin
 XX

PS Disclosure; Page 11; 15pp; German.

XX Pro-insulin is produced by treating recombinant precursor protein
 CC with a mercaptan to provide 2-10 SH residues per Cys residue, in
 CC presence of a chaotropic agent and in aq. medium of pH 10-11,
 CC treating the prod. with 3-50 g hydrophobic adsorber resin per 1 aq.
 CC medium of pH 4-7, isolating the adsorbed resin and pro-insulin and
 CC desorbing the pro-insulin. This method produces pro-insulin with
 CC correctly bonded Cys bridges. Compared with known methods it
 CC involves fewer stages (esp. no sulphitolysis or cyanogen bromide
 CC cleavage) and overall losses during purification are reduced, i.e.
 CC the process is quicker and gives better yields.
 CC Sequences of insulin chain A, B and C are given in AAR68895-97.
 CC Sequences of pro-insulin 1-4 are given in AAR68898-901.

XX Sequence 96 AA;

Query Match 96.2%; Score 152; DB 15; Length 96;
 Best Local Similarity 96.9%; Pred. No. 6.3e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPTSSSTKTKTQLEHLLKQLMILNGINNY 32
 DB 1 MAPTSSSTKTKTQLEHLLKQLMILNGINNY 32

RESULT 9

AAR78662
 ID AAR78662 standard; protein; 96 AA.

AC AAR78662;

DT 03-APR-1996 (first entry)

DE Fusion protein contg. proinsulin sequence 3.

XX Proinsulin; post-translational modification; recombinant production;
 KW protein folding; conformation.

XX Synthetic.

FH Key Location/Qualifiers
 FT Region 41..44
 FT /label= R2

FT Peptide /note= "a peptide of 4 amino acids"
 FT 45..74
 FT /label= R1-(B2-B29)-Y

FT Region /note= "human insulin B-chain"
 FT 75
 FT /label= X

FT Peptide /note= "human insulin A-chain"
 FT 76..96
 FT /label= Gly-(A2-A20)-R3

XX EP68292-A2.

XX

XX

XX

XX

XX

PF 09-FEB-1995; 95EP-0101748.
 XX
 PR 18-FEB-1994; 94DE-4405179.
 XX
 PA (FARH) HOECHST AG.
 XX
 PI Gerl M, Ludwig J, Obermeier R, Sabel W;
 XX
 XX WPI; 1995-284754/38.

PT Isolation of insulin that is correctly post-translationally
 PT processed - by reacting pro-insulin with a mercaptan in the presence
 PT of a chaotropic agent and purificn. after absorption to hydrophobic
 PT resin
 XX

PS Example 2; Page 8; 16pp; German.

XX The present sequence is that of a fusion protein, produced in E.coli
 CC which contains an example of a proinsulin molecule corresp.
 CC to the general formula R2-R1-(B2-B29)-Y-X-Gly-(A2-A20)-R3 (II). In
 CC formula (II), X = Lys, Arg or a peptide of 2-35 amino acids contg.
 CC Lys or Arg at the N- and C-termini; Y = a natural amino acid; R1 =
 CC Phe or a bond; R2 = H, Arg, Lys, a peptide of 2-45 amino acids
 CC contg. Arg or Lys at the N- and C-termini; R3 = a natural amino
 CC acid; (A2-A20) and (B2-B29) are the insulin A- and B-chain sequences
 CC from human or other insulin. The proinsulin molecule, released by
 CC cyanogen bromide, is reacted with mercaptan at a ratio of 2-10 SH
 CC residues of mercaptan per Cys residue of proinsulin. The reaction
 CC takes place in the presence of a chaotropic auxiliary agent at
 CC pH 10-11 and results in proinsulin with correctly linked cystine
 CC bridges. Reaction with trypsin and opt. carboxypeptidase B yields
 CC correctly folded insulin. The insulin is isolated by absorption on
 CC a hydrophobic resin.
 XX

SQ Sequence 96 AA;

Query Match 96.2%; Score 152; DB 16; Length 96;
 Best Local Similarity 96.9%; Pred. No. 6.3e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPTSSSTKTKTQLEHLLKQLMILNGINNY 32
 DB 1 MAPTSSSTKTKTQLEHLLKQLMILNGINNY 32

RESULT 10

AAR22595

ID AAR22595 standard; Protein; 133 AA.

XX AAR22595;

DT 03-NOV-1992 (first entry)

DE Interleukin-2 used to make hybrid proteins.

XX IL-2; hybrid; diphtheria; toxin; DT; proliferation; peripheral blood;
 KW mononuclear cells; PBMC; auto-immune response; diabetes; rheumatoid;
 KW arthritis; allograft rejection; T-suppressor.

XX Homo sapiens.

OS WO9206117-A.

PN 16-APR-1992.

PD 27-SEP-1991; 91WO-US07342.

PF 28-SEP-1990; 90US-0590113.

XX (SERA-) SERAGEN INC.

XX (UYHO-) UNIVERSITY HOSPITAL.

XX Murphy JR, Svrluga R;

XX WPI; 1992-150820/18.
 DR N-PSDB; AAQ23867.
 XX Hybrid protein comprising portion of the IL-2 binding domain -
 PT useful for inhibiting unwanted immune responses e.g. autoimmune
 PT diseases and reaction to organ and tissue transplants
 XX Disclosure; Fig 1; 37pp; English.
 PS The interleukin-2 protein is part of a hybrid protein comprising
 CC the binding domain of IL-2 and an enzymatically inactive fragment
 CC of diphtheria toxin which does not include a functional DT
 CC generalised eukaryotic binding site (see AAR26486). The hybrid
 CC protein is capable of stimulating the proliferation of peripheral
 CC blood mononuclear cells in vitro and of suppressing an immune
 CC response in a mammal in vivo. The hybrid protein allows the
 CC inhibition of an unwanted immune response such as autoimmune disease,
 CC e.g. diabetes and rheumatoid arthritis, or allograft rejection. It
 CC does not cause general immunosuppression, so avoids the resulting
 CC risk of life threatening infections. In the treatment of allograft
 CC rejection the hybrid protein spares donor-specific T-suppressor cells,
 CC which can thus proliferate and aid in prolonging graft survival. The
 CC hybrid protein does not need to be tailored to individual patients but
 CC can be used as a universal inhibiting agent. Therapy need not be
 CC continuous following allograft or an acute stage of autoimmune
 CC disease, but can be discontinued after a course of treatment.
 XX
 SQ Sequence 133 AA;
 Query Match 96.2%; Score 152; DB 13; Length 133;
 Best Local Similarity 96.9%; Pred. No. 9e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAPSSSTKKTQLQLEHLLKLMILNGINNY 32
 DB 1 MAPSSSTKKTQLQLEHLLKLMILNGINNY 32
 RESULT 11
 AAP40050
 ID AAP40050 standard; Protein; 134 AA.
 XX AAP40050;
 AC
 DT 14-JAN-1992 (first entry)
 XX
 DE Sequence of an interleukin-2-like polypeptide encoded by the DNA
 DE insert of pSV-hIL2-O or pSV-hIL2-1.
 XX
 KW Diagnosis; therapy; cancer; tumour-specific cytotoxic cell; AIDS;
 KW multiple sclerosis; lupus; rheumatoid arthritis; herpes;
 KW viral disease; lymphokine.
 XX
 OS Homo sapiens.
 XX
 XX EPI18977-A.
 XX
 PD 19-SEP-1984.
 XX
 XX 25-JAN-1984; 84EP-0300439.
 PF
 XX 10-JUN-1983; 83GB-0015981.
 PR 08-FEB-1983; 83GB-0003383.
 XX
 XX (BIOJ) BIOGEN NV.
 PA
 XX Fiers WC, Devos RR;
 PI
 XX WPI; 1984-232548/38.
 DR N-PSDB; AAN40042.
 DR
 XX Prodn. of human Interleukin 2-like polypeptide(s) - useful

PT instead of IL-2 for stimulating the immune system etc.
 XX Claim 6; Page 57-58; 69pp; English.
 XX The DNA sequence is esp. selected from a human chromosomal gene bank,
 CC e.g. it is a hIL-2 related portion of lamda CH4A-ghIL-2-1 or -2, or
 CC of lamda L47-ghIL-2-1, -2 or -3. Transformed hosts are also claimed,
 CC esp. E.coli, Ps spp., B.subtilis, B.stearothermophilus. IL-2-like
 CC polypeptides are also claimed.
 XX
 SQ Sequence 134 AA;
 Query Match 96.2%; Score 152; DB 5; Length 134;
 Best Local Similarity 96.9%; Pred. No. 9.1e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAPSSSTKKTQLQLEHLLKLMILNGINNY 32
 DB 1 MAPSSSTKKTQLQLEHLLKLMILNGINNY 32
 RESULT 12
 AAP50053
 ID AAP50053 standard; Protein; 134 AA.
 XX AAP50053;
 AC
 DT 16-AUG-2002 (updated)
 DT 03-SEP-1991 (first entry)
 XX
 DE Sequence I of new biologically active Interleukin 2 (IL-2).
 XX Immunological agent; lymphokine.
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN EPI63249-A.
 XX
 PD 04-DEC-1985.
 XX
 PF 28-MAY-1985; 85EP-0113324.
 XX
 PR 29-MAY-1984; 84DE-3419995.
 XX
 XX (FARH) HOECHST AG.
 PA
 XX Engels J, Uhlmann E, Wengenmayer F, Mullner H, Winnacker EL;
 PI Mertz R, Okazaki H;
 XX
 DR WPI; 1985-304738/49.
 DR N-PSDB; AAN50037.
 XX
 PT New biologically active interleukin 2 fragments and derivs. - and
 PT coding DNA sequences, intermediate oligo-nucleotide(s), hybrid
 PT plasmid(s) and transformed cells
 XX
 PS Disclosure; Page 18-20; 33pp; German.
 XX
 CC DNA SQs coding for AAs 1-133 and 0-133 (an additional Met) of IL-2
 CC are claimed, including the CDS of SQ 1 (see AAN50037) with/without 1
 CC or 2 stop codons. The use of a synthetic gene is esp. convenient
 CC for expression in E. coli and allows modification of the AA SQ to
 CC improve peptide stability, solubility or activity. The synthetic
 CC gene was made from a series of oligonucleotides ligated to form four
 CC larger fragments designated IL 2-I to 2-IV (see AAN50038).
 CC (Updated on 16-AUG-2002 to add missing OS field.)
 XX
 SQ Sequence 134 AA;
 Query Match 96.2%; Score 152; DB 6; Length 134;
 Best Local Similarity 96.9%; Pred. No. 9.1e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTQLEHLLKQLMILGINNY 32
 DB 1 MAPSSSTKKTQLEHLLKQLMILGINNY 32

RESULT 13

AAP50855
 ID AAP50855 standard; Protein; 134 AA.

XX AC AAP50855;

XX DT 03-OCT-2002 (updated)

XX DT 01-DEC-1991 (first entry)

XX DE Sequence encoded by synthetic interleukin II (IL-2) gene.

XX KW Immunotherapy; lymphokine; interleukin-2; thymocyte mitogenesis.

XX OS Synthetic.

XX PN W08500817-A.

XX PD 28-FEB-1985.

XX PF 09-AUG-1984; 84WO-US01252.

XX PR 03-AUG-1984; 84US-0635941.

XX PR 10-AUG-1983; 83US-0521967.

XX PA (AMGE-) AMGEN.

XX PI Souza LM, Stabinsky Y;

XX WPI; 1985-062280/10.

XX DR N-PSDB; AAN50535.

XX PT Microbial expression of interleukin II and analogues - by using

XX PT manufactured DNA sequences to transform microorganisms

XX PS Example; Table IV, Page 15-16; 39pp; English.

XX CC The inventors claim a manufactured gene for the prodn. of IL-2 and

XX CC analogues, and for polypeptides of IL-2 and analogues, and for

XX CC methods for their recombinant production.

XX CC (Updated on 03-OCT-2002 to add missing OS field.)

XX SQ Sequence 134 AA;

Query Match 96.2%; Score 152; DB 6; Length 134;

Best Local Similarity 96.9%; Pred. No. 9,le-14;

Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTQLEHLLKQLMILGINNY 32

DB 1 MAPSSSTKKTQLEHLLKQLMILGINNY 32

RESULT 14

AAP61102
 ID AAP61102 standard; Protein; 134 AA.

XX AC AAP61102;

XX DT 09-MAR-1992 (first entry)

XX DE Sequence of mature human interleukin 2 (IL2) encoded by SUN-IL2.

XX KW Yeast expression vector; lymphokine.

XX OS Homo sapiens.

XX PN EP171000-A.

XX

PD 12-FEB-1986.

XX PF 26-JUL-1985; 85EP-0109405.

XX PR 27-JUL-1984; 84JP-0157038.

XX PA (SUNR) SUNTORY LTD.

XX PI Oshima T, Tanaka S, Tsujimoto M, Nakazato H;

XX WPI; 1986-043554/07.

XX DR N-PSDB; AAN60198.

XX PT Protein and peptide prodn. by immobilised yeast transformant -

XX PT contg. expression vector which induces secretion of prod. from

XX PT cell into culture medium

XX PS Disclosure; Fig 6 and Page 31; 53pp; English.

XX CC The inventors claim a method for the prodn. of a substance having

XX CC the AA SQ of AAP61102. The method uses a synthetic DNA SQ (AAN60198). A

XX CC composition contg. a protein having human IL2 activity which is

XX CC produced by the method is also claimed. The method uses yeast

XX CC transformed by a secretory expression vector.

XX SQ Sequence 134 AA;

Query Match 96.2%; Score 152; DB 7; Length 134;

Best Local Similarity 96.9%; Pred. No. 9,le-14;

Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTQLEHLLKQLMILGINNY 32

DB 1 MAPSSSTKKTQLEHLLKQLMILGINNY 32

RESULT 15

AAP70585

ID AAP70585 standard; protein; 134 AA.

XX AC AAP70585;

XX DT 10-APR-1991 (first entry)

XX DE Sequence of human interleukin-2 (IL-2).

XX KW Lymphokine.

XX OS Homo sapiens.

XX PN DE3541856-A.

XX PD 04-JUN-1987.

XX PF 27-NOV-1985; 85DE-3541856.

XX PR 27-NOV-1985; 85DE-3541856.

XX PA (FARH) HOECHST AG.

XX PI Habermann P, Wengenmayer F;

XX DR WPI; 1987-157830/23.

XX DR N-PSDB; AAN70931.

XX PT Fusion proteins contg. interleukin 2 aminoacid sequences - as

XX PT well as genes coding for these proteins, vectors contg. the

XX PT genes, and host cells contg. the vectors

XX PS Example; pp 7-8; 20pp; German.

XX CC Prefd. fusion proteins are of formula Met-X-Y-Z or Met-Z-Y-X. Where

